



STIC Search Report

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STIC Database Tracking Number: 169483

TO: David Lukton
Location: rem/3B75/3C18
Art Unit: 1654
Oct 26, 2005
Case Serial Number: 10/014147

From: P. Sheppard
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Search Notes

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SEARCH REQUEST FORM
(STIC)

10/25/05 ME

Requestor's Name: David Lukton Examiner number: 71263 Date:

Art Unit: 1654 Phone number: 571-272-0952 Serial Number: 10-014147

Mail Box: 3-C-18 Examiner Rm: 3-B-75 Results format: paper

Title: SYNTHETIC PEPTIDES THAT INHIBIT LEUKOCYTE SUPEROXIDE ANION
PRODUCTION AND/OR ATTRACT LEUKOCYTES

Applicants: BLECHA, FRANK; SHI, JISHU

Earliest Priority Date: 4/10/95

Please search SEQ ID NOS: 1, 2, 5, 6, and 7

RECEIVED
OCT 25 2005
TECH/CHEM DIVISION
(STIC)

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____

____ NA Sequence (#)

____ STN _____ Dialog

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____ AA Sequence (#)

____ Questel/Orbit _____ Lexis/Nexis

Searcher Location: _____

____ Structure (#)

____ Westlaw _____ WWW/Internet

Date Searcher Picked Up: _____

____ Bibliographic

____ In-house sequence systems

Date Completed: _____

____ Litigation

____ Commercial _____ Oligomer _____ Score/Length
____ Interference _____ SPDI _____ Encode/Transl
____ Other (specify)

Searcher Prep & Review Time: _____

____ Fulltext

Online Time: _____

____ Other

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Best Local Similarity 100.0%; Pred. No. 2.7e-15; Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRPPPPPPPPPPRLPPRIPGPPPPPPPPPP 39
 DB 1 RRRPPPYLPRPPPPPPPPPPRLPPRIPGPPPPPPPPPP 39

RESULT 2
 AAR99121
 ID AAR99121 standard; peptide; 39 AA.
 XX
 AC AAR99121;
 XX
 DT 28-OCT-1996 (first entry)
 XX
 DE Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.
 XX
 KW STD; sexually transmitted disease; HIV; human immunodeficiency virus;
 KW herpes simplex virus; HSV; Neisseria gonorrhoeae; Candida; Chlamydia;
 KW magainin; antimicrobial; squalamine.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 39 /note= "amidated"
 XX
 PN WO9608270-A2.
 XX
 PD 21-MAR-1996.
 XX
 PF 13-SEP-1995; 95WO-US011675.
 XX
 PR 13-SEP-1994; 94US-00305475.
 XX
 PA (MAGA-) MAGAININ PHARM INC.
 XX
 PI Jacob L, Zasloff M, Williams T, Bedi G;
 XX
 DR WPI; 1996-179725/18.
 XX
 PT Inhibiting sexually transmitted disease e.g. HIV or herpes simplex - by
 PT administering magainin antimicrobial or squalamine cpd. to inhibit
 PT transmission.
 PS Example 1; Page 32; 60pp; English.
 XX
 CC AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may be
 CC used to treat sexually transmitted diseases (STDs) caused by Chlamydia,
 CC HIV, herpes simplex virus, Neisseria gonorrhoeae or Candida infection.
 CC The peptides inhibit STDs by either killing the infectious organism,
 CC impeding the infection mechanism or interrupting the replication cycle of
 CC the organism. Squalamine (an antinosterol host defence molecule of the dog
 CC fish shark Squalus acanthias) and PGla (a frog antimicrobial peptide)
 CC analogues may also be useful in inhibiting STD infection and transmission
 XX
 SQ Sequence 39 AA;

Query Match 100.0%; Score 238; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 2.7e-15;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRPPPPPPPPPPRLPPRIPGPPPPPPPPPP 39
 DB 1 RRRPPPYLPRPPPPPPPPPPRLPPRIPGPPPPPPPPPP 39

RESULT 3
 AAR94446
 ID AAR94446 standard; peptide; 39 AA.
 XX
 AC AAR94446;
 XX

XX
 DT 05-NOV-1996 (first entry)
 XX
 DE Synducin peptide (PR-39) induces syndecan expression.
 XX
 KW Synducin; induction; expression; syndecan-1; syndecan-4; surface;
 KW mesenchymal cell; fibroblast; epithelial; PR-39; treatment; stasis;
 KW decubitus; ulcers; keloids; skin burns; ischemic tissues;
 KW hypercoagulation states; prevention; tumour metastasis; restenosis;
 KW inhibition; angiogenesis; proliferation; endothelial.
 XX
 OS Synthetic.
 XX
 PN WO9609322-A2.
 XX
 PD 28-MAR-1996.
 XX
 PF 22-SEP-1995; 95WO-US012080.
 XX
 PR 22-SEP-1994; 94US-00310722.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Gallo RL, Bernfield M;
 XX
 DR WPI; 1996-188401/19.
 XX
 PT Modulating mesenchymal interaction by administration of synducin - used
 PT in the treatment of wounds, tumours, restenosis, etc.
 XX
 PS Claim 4; Page 26; 34pp; English.
 XX
 CC The present peptide is a synducin, which induces the expression of
 CC syndecan-1 and syndecan-4 on the surface of mesenchymal cells, esp.
 CC fibroblasts and epithelial cells. The 36 N-terminal amino acids of the
 CC peptide were found to be identical to the 36 N-terminal amino acids of PR
 CC -39, a Pro and Arg rich antibacterial peptide previously found in porcine
 CC intestine (WO9222578). Synducins may be used in the treatment of stasis
 CC and decubitus ulcers, keloids, skin burns, ischemic tissues and
 CC hypercoagulation states, prevention of tumour metastasis, restenosis
 CC inhibition and endothelial cell angiogenesis and proliferation induction.
 CC Human microvascular endothelial cells were assayed for syndecan-4
 CC expression following exposure to 5 μ g wound fluid, dbcAMP (1 mM), the
 CC present peptide (10 microm) or a blank, to give respective cell surface
 CC syndecan-4 values (mOD/m in) of approx. 1.75, 1.70, 1.80 and 0.95
 XX
 SQ Sequence 39 AA;

Query Match 100.0%; Score 238; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 2.7e-15;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRPPPPPPPPPPRLPPRIPGPPPPPPPPPP 39
 DB 1 RRRPPPYLPRPPPPPPPPPPRLPPRIPGPPPPPPPPPP 39

RESULT 4
 AAW01446
 ID AAW01446 standard; peptide; 39 AA.
 XX
 AC AAW01446;
 XX
 DT 18-JUN-1997 (first entry)
 XX
 DE Leukocyte O2- production inhibitor peptide PR39.
 XX
 KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
 KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 KW tissue damage; oxygen radical; inflammatory disease; therapy.
 XX

CC oligopeptides cause selective inhibition of proteasome mediated
CC degeneration of peptides and stimulation of angiogenesis after their
CC intracellular introduction to a target cell. PR-39 derived peptides are
CC able to interact with at least the alpha7 subunit of the proteasomes, and
CC therefore alter the proteolytic activity of proteasomes such that a
CC selective increased expression of specific proteins occurs. The invention
CC includes methods for the selective inhibition of proteasome mediated
CC peptide degradation. The method provides means for stimulating
CC angiogenesis as required in living tissues and organs which have suffered
CC defects or have undergone anoxia and/or infarction, myocardial infarction
CC or chronic myocardial ischaemia of heart tissue. Examples are the
CC myocardium, skeletal or smooth muscle, artery or vein, lung, brain,
CC kidney, spleen, liver, gastrointestinal or nerve tissues, limbs, and
CC extremities. A particular example is after myocardial infarction or
CC ischaemia
XX
XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 238; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 RRRPRPPYLPRPPPPFFPRLLPRIPGPPRPPRPP 39
|||||
DB 1 RRRPRPPYLPRPPPPFFPRLLPRIPGPPRPPRPP 39
|||||

RESULT 8
AAB84690
ID AAB84690 standard; protein; 39 AA.
XX
XX AAB84690;
AC
DT
DT 17-SEP-2001 (first entry)
XX
XX Amino acid sequence of a PR-39 protein.
XX
KW PR-39; IkappaBalpha degradation; NFkappaB transcription factor;
KW myocardial infarction; chronic myocardial ischemia; heart disease;
KW anoxia.
XX
XX Unidentified.
XX
XX WO200147540-A1.
XX
XX
XX PD 05-JUL-2001.
XX
XX 27-DEC-2000; 2000WO-US035293.
XX
XX 29-DEC-1999; 99US-00474967.
XX
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX Simons M, Gao Y;
XX
XX WPI; 2001-441690/47.
XX
XX
XX Selective inhibition of IkappaBalpha degradation within targeted viable
XX cell collection, involves interacting PR-39 oligopeptide with
XX IkappaBalpha and proteasomes, and altering proteolytic activity of
XX proteasomes.
XX
XX Disclosure; Page 30; 69pp; English.
XX
XX
XX The present sequence represents a PR-39 protein. The specification
XX describes PR-39 derived peptides, which are used for selective inhibition
XX of IkappaBalpha degradation within a targeted cell collection in-situ.
XX The method is useful for selectively inhibiting IkappaBalpha protein
XX degradation in situ, decreasing the activity of NFkappaB transcription
XX factor and selective control of NFkappaB-dependent gene expression in
XX situ. The PR-39 derived peptides are useful in the treatment of
XX myocardial infarction, chronic myocardial ischemia of heart disease and
XX anoxia
CC

```

XX SQ Sequence 39 AA;
    Query Match      100.0%; Score 238; DB 4; Length 39;
    Best Local Similarity 100.0%; Pred. No. 2.7e-15;
    Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLRRPPPPPPPPPPRLPPRIPPGFPPRPPRFP 39
    |||||
DB 1 RRRPRPPYLRRPPPPPPPPPPRLPPRIPPGFPPRPPRFP 39

RESULT 9
ADD35364
ID ADD35364 standard; peptide; 39 AA.
XX
AC ADD35364;
XX
DT 15-JAN-2004 (first entry)
XX
DE Antimicrobial peptide PR-39.
XX
KW antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological;
KW intraocular pressure; glaucoma; ocular hypertension; hyperaemia;
KW irritation; inflammation; conjunctiva; ocular cell dysplasia;
KW iridial melanocyte hyperplasia; hyperpigmentation.
XX
OS Unidentified.
XX
WO2003079997-A2.
XX
PD 02-OCT-2003.
XX
PF 21-MAR-2003; 2003WO-US008935.
XX
PR 21-MAR-2002; 2002US-0367071P.
XX
PA (CAYM-) CAYMAN CHEM CO.
XX
PI Maxey KM, Johnson J;
XX
WPI; 2004-011506/01.
XX
PT Ophthalmic solution useful for the treatment of increased intraocular
PT pressure comprises a prostaglandin of the F-series and an antimicrobial
PT peptide.
XX
PS Disclosure; Page 11; 11pp; English.
XX
CC The invention relates to a novel ophthalmic solution comprising a
CC prostaglandin of the F-series and an antimicrobial peptide. A solution of
CC the invention has hypotensive and ophthalmological activity. The solution
CC is useful for the treatment of increased intraocular pressure, such as
CC caused by glaucoma and for the reduction of ocular hypertension. The
CC prostaglandin and the antimicrobial peptide work synergistically, to
CC provide beneficial reduction in the incidence of irritant and toxic side
CC effects such as hyperaemia, irritation and inflammation of conjunctiva,
CC ocular cell dysplasia, iridial melanocyte hyperplasia, and
CC hyperpigmentation, associated with the prior art prostaglandin
CC compositions. The present sequence represents an antimicrobial peptide of
CC the invention.
XX
SQ Sequence 39 AA;
    Query Match      100.0%; Score 238; DB 8; Length 39;
    Best Local Similarity 100.0%; Pred. No. 2.7e-15;
    Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLRRPPPPPPPPPPRLPPRIPPGFPPRPPRFP 39
    |||||
DB 1 RRRPRPPYLRRPPPPPPPPPPRLPPRIPPGFPPRPPRFP 39

RESULT 10
ADE86112
ID ADE86112 standard; peptide; 39 AA.
XX
AC ADE86112;
XX
DT 29-JAN-2004 (first entry)
XX
DE Proline-arginine (PR)-rich antimicrobial peptide PR-39.
XX
KW Leucocyte superoxide anion; leukocyte O2- production;
KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;
KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;
KW tissue damage; oxygen radical; antibacterial.
XX
OS Synthetic.
XX
US2003125249-A1.
XX
PD 03-JUL-2003.
XX
PF 07-DEC-2001; 2001US-00014147.
XX
PR 10-APR-1995; 95US-00419066.
PR 08-OCT-1997; 97US-00930777.
XX
PA (BLEC/) BLECHA F.
PA (SHIJ/) SHI J.
XX
PI Blecha F, Shi J;
XX
WPI; 2004-059188/06.
XX
PT Attracting leukocyte to location by administering peptide including
PT proline-arginine-rich antimicrobial peptide or its truncated analogs to
PT the location.
XX
PS Claim 2; SEQ ID NO 1; 24pp; English.
XX
CC The present invention relates to a method of inhibiting leukocyte
CC superoxide anion (O2-) production and/or attracting leukocytes. The
CC method comprises the use of proline-arginine (PR)-rich antimicrobial
CC peptides or their truncated analogues. The method is useful for
CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or
CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are
CC useful as medicaments to fight infection by attracting leukocytes to a
CC wound site, while restricting tissue damage at the wound site caused by
CC excessive oxygen radicals produced by these leukocytes. The present
CC sequence represents a PR-rich antimicrobial peptide.
XX
SQ Sequence 39 AA;
    Query Match      100.0%; Score 238; DB 8; Length 39;
    Best Local Similarity 100.0%; Pred. No. 2.7e-15;
    Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLRRPPPPPPPPPPRLPPRIPPGFPPRPPRFP 39
    |||||
DB 1 RRRPRPPYLRRPPPPPPPPPPRLPPRIPPGFPPRPPRFP 39

RESULT 11
ADL67254
ID ADL67254 standard; peptide; 39 AA.
XX
AC ADL67254;
XX
DT 20-MAY-2004 (first entry)
XX
DE Antimicrobial peptide PR-39.
XX
KW Leucocyte ; superoxide anion; oxygen radical; proline-arginine ;
KW antimicrobial; antioxidant; NADPH oxidase ; p47phox; neutrophil;

```

KW infection; wound ; tissue damage ; PR-39 peptide.
 XX Unidentified.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= PR-26_peptide
 FT Peptide 1..19
 FT /label= PR-19_peptide
 FT Peptide 1..14
 FT /label= PR-14_peptide
 FT Region 1..3
 FT /note= "Essential for antibacterial activity"
 FT Peptide 4..26
 FT /label= PR-23_peptide
 FT Peptide 11..26
 FT /label= PR-16_peptide
 FT Region 20..26
 FT /note= "Essential for antibacterial activity"
 FT Peptide 25..39
 FT /label= PR-15_peptide
 XX
 XX US2004043934-A1.
 XX
 XX 04-MAR-2004.
 XX
 XX 28-AUG-2003; 2003US-00651147.
 XX
 XX 10-APR-1995; 95US-00419066.
 PR 08-OCT-1997; 97US-00930777.
 XX
 XX (BLEC/) BLECHA F.
 PA (SHIJ/) SHI J.
 XX
 XX Blecha F, Shi J;
 PI
 XX
 XX WPI; 2004-225728/21.
 DR
 XX
 XX Inhibiting leukocyte oxygen radical production comprises contacting a
 PT leukocyte with a peptide, where the inhibition occurs as a consequence of
 PT binding between the peptide and p47phox.
 PT
 XX
 PS Claim 1; SEQ ID NO 1; 24pp; English.
 XX
 CC The invention relates to inhibiting leukocyte superoxide anion (O2-)
 CC production using a naturally occurring proline-arginine (PR)-rich
 CC antimicrobial peptide known as PR-39 and its truncated analogs. The
 CC method comprises contacting leukocytes with the peptide comprising 39 or
 CC 26 amino acids, for a time and under conditions effective to inhibit
 CC leukocyte superoxide anion production. The peptide inhibits the activity
 CC of NADPH oxidase responsible for anion production, by binding to Src
 CC homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein
 CC of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or
 CC porcine leukocyte and the mammalian leukocyte is neutrophil. Another
 CC method is also disclosed which employs a PR-39 analog that comprise 16
 CC amino acids, where the sum of the proline and arginine residues in the
 CC effective peptide is at least 66 or 74 % of the total number of amino
 CC acids. This peptide inhibits leukocyte O2- production by the effective
 CC binding to p47phox in whole cells, therefore interfering with the binding
 CC of p47phox to p22phox. At least 14 or 25% of the amino acid residues in
 CC the peptide are arginine residues. The method of the invention is useful
 CC for inhibiting leukocyte oxygen radical production. The peptides are
 CC useful as medicaments for fighting infections by attracting leukocytes to
 CC a wound site, yet restrict tissue damage at the wound site caused by
 CC excessive oxygen radicals produced by these leukocytes. The present
 CC sequence is PR-39 peptide.
 XX
 XX Sequence 39 AA;
 SQ

Query Match 100.0%; Score 238; DB 8; Length 39;
 Best Local Similarity 100.0%; Pred. No. 2.7e-15;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW
 XX 1 RRRPPPYLPRPPPPPPPPRLPPRIPPGFPFRPPPPPP 39
 DB |||||
 1 RRRPPPYLPRPPPPPPPPPPRLPPRIPPGFPFRPPPPPP 39
 |||||
 RESULT 12
 ABB07714
 ID ABB07714 standard; peptide; 42 AA.
 XX
 AC ABB07714;
 XX
 DT 10-JUN-2002 (first entry)
 XX
 DE Antimicrobial peptide PR-39 C-terminal fragment.
 XX
 KW Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response;
 KW antigen presenting cell; adjuvant; porcine; PR-39.
 XX
 OS Sus sp.
 XX
 XX WO200213857-A2.
 XX
 XX 21-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-EP009529.
 XX
 XX 17-AUG-2000; 2000AT-00001416.
 XX
 XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 XX Fritz J, Mattner F, Zauner W, Buschle M, Egyed A;
 PI
 XX WPI; 2002-269154/31.
 DR
 XX
 XX Vaccine for active immunization or for preparing an adjuvant for
 PT enhancing an immune response to at least one antigen, comprises at least
 PT one antigen and at least one cathelicidin derived antimicrobial peptide.
 PT
 XX
 PS Disclosure; Fig 3; 65pp; English.
 XX
 CC The invention relates to a vaccine comprising at least one antigen and at
 CC least one cathelicidin derived antimicrobial peptide or its derivative.
 CC The vaccine is useful for active immunization, especially of humans or
 CC animals without protection against the specific antigen. The cathelicidin
 CC derived antimicrobial peptide is useful in the preparation of an adjuvant
 CC for enhancing the immune response to at least one antigen, where the
 CC adjuvant enhances the uptake of at least one antigen in antigen
 CC presenting cells (APC), and the adjuvant is added to the vaccine.
 CC Sequences ABB07708-15 represent C-terminal fragments of antimicrobial
 CC peptides of the cathelicidin family
 XX
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 238; DB 5; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2.9e-15;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 KW
 XX 1 RRRPPPYLPRPPPPPPPPRLPPRIPPGFPFRPPPPPP 39
 DB |||||
 1 RRRPPPYLPRPPPPPPPPPPRLPPRIPPGFPFRPPPPPP 39
 |||||
 RESULT 13
 ADR82250
 ID ADR82250 standard; protein; 42 AA.
 XX
 AC ADR82250;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Cell permeation peptide bactericin.
 XX
 KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;

CC negative effect on normal mammalian and/or eukaryotic cells. The present
 CC sequence represents an AMP (antimicrobial peptide) gene amino acid
 CC sequence, which is used in an example from the present invention

XX Sequence 44 AA;

Query Match 100.0%; Score 238; DB 4; Length 44;
 Best Local Similarity 100.0%; Pred. No. 3e-15;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRRPRPPYLPRLPPRPPPPRPPRLPPRPPGPPPPRPPPP 39
 |||||
 Db 3 RRRPRPPYLPRLPPRPPPPRPPRLPPRPPGPPPPRPPPP 41
 |||||

RESULT 15

AAW01447

ID AAW01447 standard; peptide; 26 AA.

XX AC AAW01447;

XX DT 18-JUN-1997 (first entry)

XX D2 Leukocyte O2- production inhibitor peptide PR26.

XX Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
 KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 KW tissue damage; oxygen radical; inflammatory disease; therapy.

XX OS Synthetic.

XX FN WO9632129-A1.

XX PD 17-OCT-1996.

XX PF 10-APR-1996; 96WO-US004674.

XX PR 10-APR-1995; 95US-00419066.

XX PA (UNIV) UNIV KANSAS STATE RES FOUND.

XX PI Blecha F, Shi J;

XX DR WPI; 1996-476842/47.

PT Inhibition of leukocyte superoxide anion prodn. and attraction of
 PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.

XX PS Claim 3; Page 26; 45pp; English.

XX AAW01447-W01454 represent fragments of the proline-arginine rich
 CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
 CC isolated from porcine small intestine, and has also been identified in
 CC human and porcine neutrophils. PR39 kills bacteria by interfering with
 CC DNA and/or protein synthesis. PR39 also induces syndecan expression on
 CC mesenchymal cells. Syndecans are important in wound repair, showing that
 CC PR39 can be used in wound repair, as well as in antibacterial agents.
 CC These sequences, and PR39, can be used in the method of the invention.
 CC The method of the invention is for inhibiting leukocyte superoxide anion
 CC (O2-) production. The method comprises administering to a leukocyte a
 CC peptide (such as this sequence) capable of inhibiting leukocyte O2-
 CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting tissue
 CC damage at the wound site caused by excessive oxygen radicals produced by
 CC these leukocytes. They can also be used to develop products for treating
 CC inflammatory disease states

XX SQ Sequence 26 AA;

Query Match

65.1%; Score 155; DB 2; Length 26;

Best Local Similarity

100.0%; Pred. No. 8.7e-08;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRRPRPPYLPRLPPRPPPPRPPRLPPRPPGPPPPRPPPP 26
 |||||
 Db 1 RRRPRPPYLPRLPPRPPPPRPPRLPPRPPGPPPPRPPPP 26
 |||||

Search completed: October 26, 2005, 05:12:03
 Job time : 158.518 secs

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:00:14 ; Search time 29,0727 Seconds
(without alignments)
129,071 Million cell updates/sec

Title: US-10-014-147-1
Perfect score: 238
Sequence: 1 RRRPPVLP RRRPPPPPPPPRLPPRI PPGFPFRFPFP 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: piri:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	238	100.0	172	2 S68232	antimicrobial prot
2	122.5	51.5	199	2 S14981	extensin class I (
3	109.5	46.0	212	2 S57330	cathelin-like anti
4	107	45.0	301	2 J01663	hybrid proline-ric
5	105.5	44.3	397	2 T28872	hypothetical prote
6	102.5	43.1	228	2 S40463	prophenin (PF-2) p
7	98.5	41.4	42	2 B36589	bactenecin 5 - bov
8	98	41.2	1006	2 G86292	hypothetical prote
9	97.5	41.0	134	2 D84672	hypothetical prote
10	95	39.9	439	2 S51939	chitinase (EC 3.2.
11	94.5	39.7	221	2 T07176	extensin homolog -
12	94.5	39.7	382	2 T39068	proline-arginine
13	94	39.5	176	2 A45328	bactenecin 5 precu
14	93	39.1	59	2 A36589	bactenecin 7 - bov
15	92.5	38.9	148	2 S39206	proline-rich prote
16	92.5	38.9	547	2 C96828	unknown protein F1
17	92	38.7	494	2 B96534	hypothetical prote
18	92	38.7	1460	1 ED8E1F	immediate-early pr
19	91.5	38.4	1560	2 T42727	proliferation pote
20	91	38.2	134	2 JC5572	proline-rich prote
21	91	38.2	424	2 A54964	spliceosome-associ
22	90.5	38.0	388	2 JC5437	epilysin
23	90.5	38.0	574	2 T43556	Wiskott-Aldrich sy
24	90.5	38.0	574	2 T38819	wiskott-aldrich sy
25	90.5	38.0	948	2 A57640	retinoblastoma bin
26	90	37.8	329	2 T10064	cytokinin-induced
27	89	37.4	141	2 A34043	hypothetical proli
28	89	37.4	599	2 T10798	phosphorin-S - Vo
29	88.5	37.2	1958	2 B40505	hypothetical prote

30	88	37.0	485	2 A33647	sulfated surface g
31	87.5	36.8	1098	2 T08599	probable transcript
32	87	36.6	196	2 B48232	cysteine-rich exte
33	87	36.6	381	2 S52985	cell wall protein
34	87	36.6	487	2 S24442	nuclear protein B3
35	87	36.6	1206	2 S24407	formin isoform IV
36	87	36.6	1468	2 S11515	formin - mouse
37	86.5	36.3	1268	2 T31420	C-terminal domain-
38	86	36.1	57	2 S10782	salivary protein p
39	86	36.1	79	1 PQHUSB	proline-rich pepti
40	86	36.1	322	2 S09779	hypothetical prote
41	86	36.1	367	1 OZZQMY	circumsporozoite p
42	86	36.1	415	1 A34170	acrosin (EC 3.4.21
43	86	36.1	431	2 S47538	acrosin (EC 3.4.21
44	86	36.1	449	2 D87682	OmpA family protei
45	86	36.1	620	2 S06733	hydroxyproline-ric

ALIGNMENTS

RESULT 1

S68232
antimicrobial protein PR-39 precursor, cathelin-associated - pig
N/Alternate names: myeloid antibacterial protein PR-39
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S68232; JN0899; I47138; S19563
R/Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 376, 130-134, 1995
A/Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni
A/Reference number: S68232; MUID:96105365; PMID:7498526
A/Accession: S68232
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-172 <ZHA>
A/Cross-references: UNIPROT:P80054; EMBL:X89201; NID:g1165150; PIDN:CAA61487.1; PID:g116:
A/Experimental source: leukocytes
R/Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
A/Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the i
A/Reference number: JN0899; MUID:94071853; PMID:8250863
A/Accession: JN0899
A/Molecule type: mRNA
A/Residues: 1-20, 'A', 22-172 <STO>
A/Cross-references: GB:I23825; NID:9435100; PIDN:AAA31109.1; PID:G435101
A/Experimental source: bone marrow cells
R/Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bone
proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
A/Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fam
A/Reference number: I47138; MUID:95350216; PMID:7624374
A/Accession: I47138
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-28, 'T', 30-89, 'OR', 92-116, 'NDP', 120-172 <GUD>
A/Cross-references: EMBL:X87236; NID:9829142; PIDN:CAA60682.1; PID:g1051298
R/Agarberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall,
Eur. J. Biochem. 202, 849-854, 1991
A/Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of th
A/Reference number: S19563; MUID:92111534; PMID:1765098
A/Accession: S19563
A/Molecule type: protein
A/Residues: 131-169 <AGE>
A/Experimental source: intestine
C/Genetics:
A/Gene: PR39
A/Introns: 66/3; 102/3; 126/3
C/Superfamily: cathelin; cystatin homology
C/Keywords: amidated carboxyl end; antibacterial
F/1-29/Domain: signal sequence #status predicted <SIG>
F/22-129/Domain: cystatin homology <CYS>
F/30-130/Domain: propeptide #status predicted <PRO>
F/131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>

F:169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

```
Query Match      100.0%; Score 238; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPVPLRRPPPPPPPPPPRLPRIPGPPPPPPPPPP 39
    |||||
DB 131 RRRPPVPLRRPPPPPPPPPPRLPRIPGPPPPPPPP 169

RESULT 2
S14981
extensin class I (clone w1-8 L) - tomato (fragment)
C:Species: Lycopersicon esculentum (tomato)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 11-Jan-2000
C:Accession: S14981
R:Shewalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
Plant Mol. Biol. 16, 547-565, 1991
A:Title: Tomato extensin and extensin-like cDNAs: structure and expression in response to
A:Reference number: S14970; MUID:91329690; PMID:1714316
A:Accession: S14981
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-199 <SHO>
A:Cross-references: EMBL:X55692
A:Experimental source: cv. UC82B
C:Superfamily: hydroxyproline-rich glycoprotein
C:Keywords: cell wall; glycoprotein; hydroxyproline

Query Match      51.5%; Score 122.5; DB 2; Length 199;
Best Local Similarity 57.9%; Pred. No. 0.00019;
Matches 22; Conservative 3; Mismatches 10; Indels 3; Gaps 1;

QY 2 RRPVPLRRPPPPPPPPPPRLPRIPGPPPPPPPP 36
    |||||
DB 69 RRPVPLRRPPPPPPPPPPRLPRIPGPPPPPPPP 106

RESULT 3
S57330
cathelin-like antibacterial peptide precursor (clone C6) - pig (fragment)
N:Alternate names: antimicrobial peptide; prophenin-1
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S57330; S68726
R:Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V.
Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
A:Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte
A:Reference number: S57330; MUID:96042752; PMID:7576250
A:Accession: S57330
A:Molecule type: mRNA
A:Residues: 1-212 <STR>
A:Cross-references: UNIPROT:P51524; GB:X86031; NID:gl006756; PIDN:CAA60023.1; PID:gl0067
R:Harwig, S.S.L.; Kokryakov, V.N.; Swiderek, K.M.; Aleshina, G.M.; Zhao, C.; Lehrer, R.I.
FEBS Lett. 362, 65-69, 1995
A:Title: Prophenin-1, an exceptionally proline-rich antimicrobial peptide from porcine l
A:Reference number: S68726; MUID:95212585; PMID:7690355
A:Accession: S68726
A:Molecule type: protein
A:Residues: 131-209 <HAR>
A:Experimental source: leukocytes
C:Superfamily: cathelin; cystatin homology
C:Keywords: antibacterial
F:6-113/Domain: cystatin homology <CVS>

Query Match      46.0%; Score 109.5; DB 2; Length 212;
Best Local Similarity 53.7%; Pred. No. 0.0028;
Matches 29; Conservative 1; Mismatches 5; Indels 19; Gaps 6;

QY 2 RRPVPLRRPPPPPPPPPPRLPRIPGPPPPPPPP 39
    |||||
DB 123 RRPVPLRRPPPPPPPPPPRLPRIPGPPPPPPPP 173

RESULT 4
JQ1663
hybrid proline-rich protein - maize
C:Species: Zea mays (maize)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JQ1663
R:Jose-Estanyol, M.; Ruiz-Avila, L.; Puigdomenech, P.
Plant Cell 4, 413-423, 1992
A:Title: A maize embryo-specific gene encodes a proline-rich and hydrophobic protein.
A:Reference number: JQ1663; MUID:92361259; PMID:1498600
A:Accession: JQ1663
A:Molecule type: DNA
A:Residues: 1-301 <JOS>
A:Cross-references: UNIPROT:Q41848; EMBL:X60432; NID:G433706; PIDN:CAA42959.1; PID:G43370
A:Experimental source: strain W64A
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match      45.0%; Score 107; DB 2; Length 301;
Best Local Similarity 50.0%; Pred. No. 0.0064;
Matches 21; Conservative 3; Mismatches 12; Indels 6; Gaps 2;

QY 4 PRPPVPLRRPPPPPPPPPPRLPRIPGPPPPPPPP 39
    |||||
DB 169 PRPPVPLRRPPPPPPPPPPRLPRIPGPPPPPPPP 210

RESULT 5
T28872
hypothetical protein R04E5.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28872
R:Miller, N.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid R04E5.
A:Reference number: Z20535
A:Accession: T28872
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-997 <ML>
A:Cross-references: UNIPROT:Q9GYL4; EMBL:U41538; PIDN:AAC48181.1; GSPDB:GN00028; CESP:R04
A:Experimental source: strain Bristol N2; clone R04E5
C:Genetics:
A:Gene: CESP:R04E5.8
A:Map position: X
A:Introns: 216/3; 234/3; 255/2; 305/1; 669/3; 891/1; 986/2

Query Match      44.3%; Score 105.5; DB 2; Length 997;
Best Local Similarity 55.8%; Pred. No. 0.026;
Matches 24; Conservative 0; Mismatches 14; Indels 5; Gaps 2;

QY 2 RRPVPLRRPPPPPPPPPPRLPRIPGPPPPPPPP 39
    |||||
DB 145 RRPVPLRRPPPPPPPPPPRLPRIPGPPPPPPPP 187

RESULT 6
S40463
prophenin (PF-2) precursor - pig
N:Alternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S40463; S57331; S68233
R:Pungercar, J.; Strukelj, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, F.; Turk,
FEBS Lett. 336, 284-288, 1993
A:Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial l
A:Reference number: S40463; MUID:94085623; PMID:8262247
A:Accession: S40463
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-228 <PUN>
```


C:Genetics:
A:Gene: VCS-betal
A:Introns: 18/3
C:Superfamily: proline-rich peptide P-B
C:Keywords: glycoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-148/Product: proline-rich protein V-beta 1 #status predicted <MAT>
F:133,143/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.9%; Score 92.5; DB 2; Length 148;
Best Local Similarity 52.3%; Pred. No. 0.063;
Matches 23; Conservative 0; Mismatches 12; Indels 9; Gaps 3;
QY 1 RRRPPVLPDRPPPP-----FPPRLPPRIPPGPPPPPPPPPP 39
DB 32 RRRPPPP--PPPPPPPPFGIGQPP--PPHFGFGFGPPPPPPPP 71

Search completed: October 26, 2005, 05:19:57
Job time : 31.0727 secs

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RA Mutt V., Joernvall H.;
RA "Amino acid sequence of PR-39. Isolation from pig intestine of a new
RT member of the family of proline-arginine-rich antibacterial
RT peptides";
RT Eur. J. Biochem. 202:849-854 (1991).
RL [5]
RN
RP SEQUENCE OF 131-164, AND FUNCTION.
RC TISSUE=Neutrophils;
RX MEDLINE=95088504; PubMed=7996056;
RA Shi J., Ross C.R., Chengappa M.M., Blecha F.;
RA "Identification of a proline-arginine-rich antibacterial peptide from

neutrophils that is analogous to PR-39, an antibacterial peptide from the small intestine.";

RA Leukoc. Biol. 56:807-811(1994).

CC -!- FUNCTION: Exerts a potent antimicrobial activity against both E.coli and B.megaterium.

CC -!- TISSUE SPECIFICITY: Small intestine and bone marrow.

CC -!- SIMILARITY: Belongs to the cathelicidin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; X87236; AAA60682.1; -.

DR EMBL; L23825; AAA31109.1; -.

DR EMBL; X89201; CAA61487.1; -.

DR PIR; S68232; S68232.

DR HSP; P32196; IKWI.

DR InterPro; IPR001894; Cathelicidin.

DR Pfam; PF00666; Cathelicidins; 1.

DR ProDom; PD001838; Cathelicidin; 1.

DR PROSITE; PS00946; CATHELICIDINS_1; 1.

DR PROSITE; PS00947; CATHELICIDINS_2; 1.

CC Annotation; Antibiotic; Direct protein sequencing;

KW Pyrrolidone carboxylic acid; Signal.

FT SIGNAL 1 29

FT PROPEP 30 130

FT CHAIN 131 169

FT MOD_RES 30 30

FT DISULFID 85 96

FT DISULFID 107 124

FT MOD_RES 169 169

FT CONFLICT 21 21

FT CONFLICT 29 29

FT CONFLICT 90 91

FT CONFLICT 117 119

FT CONFLICT 157 157

FT CONFLICT 172 AA; 19476 MW; 994B792798C0E133 CRC64;

SQ SEQUENCE 100.0%; Score 238; DB 1; Length 172;

Query Match 100.0%; Pred. No. 3.6e-13;

Best Local Similarity 100.0%; Pred. No. 3.6e-13;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPPVLP...RRPPPPRLPRIPPGPPPPPPRFP 39

DB 131 RRRPPPPVLP...RRPPPPRLPRIPPGPPPPPPRFP 169

RESULT 2

Q8ILQ0 Q8ILQ0 PRELIMINARY; PRT; 484 AA.

AC Q8ILQ0;

DT 01-MAR-2003 (TReMBLrel. 23, Created)

DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Spliceosome-associated protein, putative.

GN ORFNames=PF14_0194;

OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=36329;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;

RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Paterford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Augiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,

RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McRadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;

RA "Genome sequence of the human malaria parasite Plasmodium falciparum";

RT Nature 419:498-511(2002).

RL EMBL; AE014819; AAN36806.1; -.

DR HSSP; P11940; ICVJ.

DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF00076; RRM_1; 2.

DR SMART; SM00360; RRM; 2.

DR PROSITE; PS0102; RRM; 2.

SQ SEQUENCE 484 AA; 53722 MW; 0858953D48F72E2B CRC64;

Query Match 53.6%; Score 127.5; DB 2; Length 484;

Best Local Similarity 62.2%; Pred. No. 0.002;

Matches 23; Conservative 0; Mismatches 11; Indels 3; Gaps 1;

QY 6 PPYP...RRPPPPPPPPRLPRIPPGPPPPPPRFP 39

DB 405 PPTLPNPPPTLPNPPPTLPNPPPPGPPNLPNPP 441

RESULT 3

Q9XIZ3 Q9XIZ3 PRELIMINARY; PRT; 333 AA.

AC Q9XIZ3;

DT 01-NOV-1999 (TReMBLrel. 12, Created)

DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Similar to Zea mays PRP gene. (X60432).

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RA Sasaki T., Nagamura Y., Yamamoto K.;

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB023482; BAA78762.1; -.

DR HSSP; P24337; IHYP.

DR Gramene; Q9XIZ3; -.

DR InterPro; IPR003612; AAI.

DR Pfam; PF00234; Tryp_alpha_aml; 1.

DR SMART; SM00499; AAI; 1.

SQ SEQUENCE 333 AA; 34823 MW; 268DEC74E20E8194 CRC64;

Query Match 49.6%; Score 118; DB 2; Length 333;

Best Local Similarity 51.2%; Pred. No. 0.009;

Matches 21; Conservative 3; Mismatches 15; Indels 2; Gaps 1;

QY 1 RRRPPPPVLP...RRPPPPRLPRIPPGPPPPPPRFP 39

DB 172 RPPTPPPVPSPPPPVPPPIPTTPPPVPPPTPPVP 212

RESULT 4

Q7RQAO Q7RQAO PRELIMINARY; PRT; 415 AA.

AC Q7RQAO;

DT 01-MAR-2004 (TReMBLrel. 26, Created)

DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Splicing factor 3b subunit 4.

GN Name=PY01202;

OS Plasmodium yoelii yoelii.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=73239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=17XNL;


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CC EMBL; X86031; CAA60023.1; -.
CC DR PIR; S57330; S57330.
CC DR HSP; P32196; ILXE.
CC DR InterPro; IPR001894; Cathelicidin.
CC DR Pfam; PF00666; Cathelcicidins_1.
CC DR ProDom; PD001838; Cathelcicidin; 1.
CC DR PROSITE; PS00946; CATHELICIDINS_1; 1.
CC DR PROSITE; PS00947; CATHELICIDINS_2; 1.
CC DR Amidation; Antibiotic; Direct protein sequencing;
KW Pyroglutamate carboxylic acid; Repeat; Signal.
FT NON_TER 1 1
FT SIGNAL <1 13 Potential.
FT FT PROPEP 14 130 Potential.
FT FT PEPTIDE 131 209 Propenin-1.
FT FT PROPEP 210 212 Removed in mature form (Potential).
FT MOD_RES 14 14 Pyrrolidone carboxylic acid (By similarity).
FT FT DISULFID 69 80 By similarity.
FT FT DISULFID 91 108 By similarity.
FT FT MOD_RES 209 209 Proline amide (G-210 provides amide group) (Potential).
FT FT DOMAIN 116 212 7 X 10 AA tandem repeats.
FT FT DOMAIN 132 201 1.
FT FT REPEAT 132 141 1.
FT FT REPEAT 142 151 2.
FT FT REPEAT 152 161 3.
FT FT REPEAT 162 171 4.
FT FT REPEAT 172 181 5.
FT FT REPEAT 182 191 6.
FT FT REPEAT 192 201 7.
SQ SEQUENCE 212 AA; 23956 MW; A315414C90DBF423 CRC64;

Query Match 46.0%; Score 109.5; DB 1; Length 212;
Best Local Similarity 53.7%; Pred. No. 0.031;
Matches 29; Conservative 1; Mismatches 5; Indels 19; Gaps 6

Oy 2 RRPR-----PPYLRRPR-PPPFPP-PLRLPRIPGGFP-RRFP-----RRFP 39
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 123 RRPRLRQARPPPNVPGRRPPPNFGRRFP---PPNPPGRFPNPPNPPGRFP 173

RESULT 6
Q657Y0 PRELIMINARY; PRT; 236 AA.
AC Q657Y0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0005A05.30 (Hypothetical protein
DE P0482C06.8).
DE Name=P0005A05.30; Synonyms=P0482C06.8;
GN Oryza sativa [japonica cultivar-group].
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arioka K., Chiden Y., Hayaashi M.,
RA Okamoto M., Ando T., Aoki H., Arica K., Hamada M., Hazada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Tijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saiji S., Sakai K., Shibata M.,
RA Shinokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
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RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP002863; BAD44889.1; -.
DR EMBL; AP002845; BAD44850.1; -.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 24666 MW; DAC94868D2903ED2 CRC64;

Query Match 45.6%; Score 108.5; DB 2; Length 236;
Best Local Similarity 51.0%; Pred. No. 0.041;
Matches 25; Conservative 1; Mismatches 10; Indels 13; Gaps 2;

Qy 2 RRPDPY-----LPRRPPPPPPRLPPRI-----PPGPPPPPPR 37
:||||| :||||| :||||| :||||| :||||| :|||||
Db 52 RQRPPLAHPPLPLVLRPLPLPLVLRPLQLAAGPPGPPRGRPR 100

RESULT 7
ID O61649 PRELIMINARY; PRT; 93 AA.
AC O61649;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pyrolidone-rich antigen.
GN Name=Ov42;
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RA Titanji V.P.K., Souopgui J., Goghomu S.M., Nde P.N., Lucius R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF055985; AAC12760.1; -.
SQ SEQUENCE 93 AA; 9785 MW; 80C22E80DE27D17 CRC64;

Query Match 45.2%; Score 107.5; DB 2; Length 93;
Best Local Similarity 57.5%; Pred. No. 0.021;
Matches 23; Conservative 0; Mismatches 12; Indels 5; Gaps 1;

Qy 5 RPPYLPRLPPPPPPPPRLPPRIPPGFP-----RPPPRFP 39
||||| :||||| :||||| :||||| :|||||
Db 21 RPPTTPTTPPPPPPPGFPRIPPFPPIQGRASFPFPFP 60

RESULT 8
ID Q41848 PRELIMINARY; PRT; 301 AA.
AC Q41848;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prolin rich protein.
GN Name=PRP;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W64A;
RX MEDLINE=92361259; PubMed=1498600;
RA Jose-Estanyol M., Ruiz-Avila L., Puigdomenech P.;
RT "A maize embryo-specific gene encodes a proline-rich and hydrophobic
protein.";
RL Plant Cell 4:413-423(1992).
DR EMBL; X60432; CAA42959.1; -.
DR PIR; JQ1663; JQ1663.
DR HSSP; P24337; 1HYP.
DR InterPro; IPR003612; AAI.

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DR Pfam; PF00234; Tryp_alpha_aml1; 1.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 301 AA; 31647 MW; 884EB70854D28C2E CRC64;

Query Match 45.0%; Score 107; DB 2; Length 301;
Best Local Similarity 50.0%; Pred. No. 0.07;
Matches 21; Conservative 3; Mismatches 12; Indels 6; Gaps 2;

Qy 4 PRPPYL---PRPPPPPPPPRLPPR---IPGFPFPFPFPFP 39
||||| :||||| :||||| :||||| :|||||
Db 169 PTPVPVPTPSPSPVPVPVPTPSPSPVPVPVPTPSP 210

RESULT 9
ID Q9SBM1 PRELIMINARY; PRT; 409 AA.
AC Q9SBM1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hydroxyproline-rich glycoprotein DZ-HRGP precursor.
GN Name=HRGP gene;
OS Volvox carteri f. nagariensis.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Volvocaceae; Volvox.
OX NCBI_TaxID=3068;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HK10;
RX MEDLINE=20044763; PubMed=10574980; DOI=10.1074/jbc.274.49.35023;
RA Ender F., Hallmann A., Amon P., Sumper M.;
RT "Response to the sexual pheromone and wounding in the green alga
RT Volvox: induction of an extracellular glycoprotein consisting almost
RT exclusively of hydroxyproline.";
RL J. Biol. Chem. 274:35023-35028(1999).
DR EMBL; AJ242540; CAB62280.1; -.
DR GO; GO:0005199; F:structural constituent of cell wall; IEA.
DR InterPro; IPR003882; PstII_extensin.
DR PRINTS; PR01218; PSTLEXTENSIN.
KW SIGNAL.
FT CHAIN 1 18 hydroxyproline-rich glycoprotein DZ-HRGP.
SQ SEQUENCE 409 AA; 41547 MW; CD0749C6AF02BD74 CRC64;

Query Match 44.5%; Score 106; DB 2; Length 409;
Best Local Similarity 60.6%; Pred. No. 0.11;
Matches 20; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 4 PRPPYLPRLPPPPPPPPRLPPRIPPGFPFPFPFP 36
||||| :||||| :||||| :||||| :|||||
Db 178 PSPPPSPPPPPPPPPPPPPPPPPPPPPPPPPPP 210

RESULT 10
ID Q9GYL4 PRELIMINARY; PRT; 997 AA.
AC Q9GYL4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein R04E5.8.
GN Name=R04E5.8; ORFNames=R04E5.8;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";

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RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Miller N.;
RT "The sequence of C. elegans cosmid R04E5."
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41538; AAG00010.1; -.
DR PIR; T28872; T28872.
DR WormBase; WGenes00019871; R04E5.8.
DR WormPep; R04E5.8a; C904800.
DR Hypothetical protein.
SQ SEQUENCE 997 AA; 111954 MW; F1620378F0D9DB6 CRC64;

Query Match 44.3%; Score 105.5; DB 2; Length 997;
Best Local Similarity 55.8%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 14; Indels 5; Gaps 2;

QY 2 RRPR--PPYLRPPPPPPPP---RLPPRPPGPPPPPPPP 39
DB 145 RVPTPPSPRRPPPPPPPPSPQRPPRTTSPSPRPRTPT 187

RESULT 11
Q84Q90 PRELIMINARY; PRT; 351 AA.
AC Q84Q90;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein QJ1041F02.15.
GN Name=QJ1041F02.15;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,
RA Collura K.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN EMBL; AC135206; AAP06858.1; -.
DR Gramine; Q84Q90; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003876; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR000690; Znf_matrin.
DR InterPro; IPR003604; Znf_U1.
DR SMART; SM00355; Znf_C2H2_1.
DR SMART; SM00451; Znf_U1; 1.
DR PROSITE; PSS0171; ZF_MATRIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 351 AA; 38984 MW; 4DE76B97D657701B CRC64;

Query Match 43.3%; Score 103; DB 2; Length 351;
Best Local Similarity 57.6%; Pred. No. 0.18;

Matches 19; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 PRPPYLRPPPPPPPPPPPPRLPPRPPGPPPPPP 36
DB 265 PRPPPPQVPPPPPPQAPPPPPNAPMGPPRIPP 297

RESULT 12
PF12_PIG STANDARD; PRT; 228 AA.
AC P51525;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Prophenin-2 precursor (PF-2) (PR-2) (C12) (Prophenin-1 like).
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=94085623; PubMed=8262247; DOI=10.1016/0014-5793(93)80821-B;
RA Pungercar J., Strukelj B., Kopitar G., Renko M., Lenarcic B.,
RA Gubensek F., Turk V.;
RT "Molecular cloning of a putative homolog of proline/arginine-rich
RT antibacterial peptides from porcine bone marrow."
RL FEBS Lett. 336:284-288(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;
RA Zhao C., Ganz T., Lehrer R.I.;
RT "Structures of genes for two cathelin-associated antimicrobial
RT peptides: prophenin-2 and PR-39."
RL FEBS Lett. 376:130-134(1995).
CC -!- FUNCTION: Exerts antimicrobial activity. It is more effective
CC against Gram-negative bacteria than Gram-positive bacteria.
CC -!- SIMILARITY: Belongs to the cathelicidin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; X75438; CAA53188.1; -.
CC EMBL; X89202; CAA61488.1; -.
CC PIR; S40463; S40463.
CC HSSP; P32196; LKWI.
CC InterPro; IPR001894; Cathelicidin.
CC Pfam; PF00666; Cathelicidins; 1.
CC ProDom; PD001838; Cathelicidin; 1.
CC PROSITE; PS00946; CATHELICIDINS 1; 1.
CC PROSITE; PS00947; CATHELICIDINS 2; 1.
KW Amidation; Antibiotic; Pyrrolidone carboxylic acid; Repeat; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 146 Potential.
FT PEPTIDE 147 225 Prophenin-2.
FT PROPEP 226 228 Removed in mature form (Potential).
FT MOD_RES 225 225 Proline amide (G-226 provides amide
FT group) (Potential).
FT DOMAIN 132 228 Pro-rich.
FT DOMAIN 148 217 7 X 10 AA tandem repeats.
FT REPEAT 148 157 1.
FT REPEAT 158 167 2.
FT REPEAT 168 177 3.
FT REPEAT 178 187 4.
FT REPEAT 188 197 5.
FT REPEAT 198 207 6.
FT REPEAT 208 217 7.

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FT	MOD_RES	30	30	Pyrrolidone carboxylic acid (By similarity).
FT	DISULFID	85	96	By similarity.
FT	DISULFID	107	124	By similarity.
SEQ	SEQUENCE	228 AA;	25855 MW; 1EA4511FF35CC182 CRC64;	
Query Match		43.1%;	Score 102.5; DB 1; Length 228;	
Best Local Similarity		51.9%;	Pred. No. 0.13;	
Matches	28; Conservative	1; Mismatches	6; Indels	19; Gaps
QY	2	RRPR-----PPVLPRRP-PPPPFP-PRLPRIIPGGFP-PRFP-----PRFP	39	
DB	139	RRRLRLRQAAPPNNVPGRRPPPPNVGPRFP---PPNFPGRFPFPNPGPRFP	189	
RESULT 13				
Q6PD05				
ID	Q6PD05	PRELIMINARY;	PRT;	640 AA.
AC	Q6PD05			
DT	05-JUL-2004	(TrEMBLrel. 27, Created)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein zgc:77390;			
GN	ORFNames=zgc:77390;			
OS	Brachydanio rerio (Zebrafish).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RP	SEQUENCE FROM N.A.			
RP	SEQUENCE=Embryo;			
RC	MEDLINE=22348257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,			
RA	Datschenko L., Marusina K., Farmer A.C., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uadin T.B., Toehiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RA	Strausberg R.;			
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC065662; AAH65662.1; -			
DR	ZFIN; ZDB-GENE-040426-1829; zgc:77390.			
SW	Hypothetical protein.			
QY	SEQUENCE	640 AA; 68823 MW; 95191F8DC32BBFF9 CRC64;		
Query Match		43.1%;	Score 102.5; DB 2; Length 640;	
Best Local Similarity		57.9%;	Pred. No. 0.34;	
Matches	22; Conservative	0; Mismatches	15; Indels	1; Gaps
QY	2	RRRPPVLPRIIPPPPPPPRLPRIPRIIPGGFPFPFPFPFP	39	
DB	417	RGMPLRLP-PGPPPGRRPPGPPPPGLPPGPPPPRGP	453	
RESULT 14				

OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WS576;
RX MEDLINE=98367519; PubMed=9692967; DOI=10.1021/bi9808013;
RA Zhang Y., Brown R.D. Jr., West C.M.;
RT "Two proteins of the Dictyostelium spore coat bind to cellulose in vitro."
RL Biochemistry 37:10766-10779(1998).
DR EMBL; AF066072; AAC19124.1; --
DR DictyBase; DDB0185060; psapB.
FT NON_TER 1
FT NON_TER 135
SQ SEQUENCE 135 AA; 14829 MW; 500634A988A49408 CRC64;

Query Match 42.6%; Score 101.5; DB 2; Length 135;
Best Local Similarity 44.7%; Pred. No. 0.095;
Matches 17; Conservative 5; Mismatches 13; Indels 3; Gaps 1;

QY 5 RPYLPRPRP---PPFPRLPRIPGPPPPRPPRFP 39
Db 21 QPPTYPTQPTQPTPYPPSPYPPPYPTPTPTYP 58

Search completed: October 26, 2005, 05:18:30
Job time : 140.082 secs

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:02:04 ; Search time 40.0636 Seconds
(without alignments)
72.667 Million cell updates/sec

Title: US-10-014-147-1

Perfect score: 238
Sequence: 1 RRRPPPPVLP RRRPPPPPPPPPPRLPPRIPGFPFRPPFRFP 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB pep.*
5: /cgn2_6/prodata/1/iaa/PCUTS COMB pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	238	100.0	39	1	US-08-162-052-1
2	238	100.0	39	1	US-08-310-722-1
3	238	100.0	39	2	US-08-419-066-1
4	238	100.0	39	2	US-08-728-333-1
5	238	100.0	39	3	US-09-024-975-1
6	238	100.0	39	4	US-08-930-777A-1
7	238	100.0	39	5	PCT-US95-12080-1
8	221.5	93.1	38	4	US-09-739-535-1
9	155	65.1	26	2	US-08-419-066-2
10	155	65.1	26	3	US-09-024-975-2
11	155	65.1	26	4	US-08-930-777A-2
12	140	58.8	23	4	US-08-930-777A-3
13	116	48.7	19	4	US-08-930-777A-4
14	106	44.5	78	1	US-08-487-359-5
15	106	44.5	78	1	US-08-222-798A-5
16	101.5	42.6	311	3	US-09-179-558-66
17	101.5	42.6	311	4	US-09-722-825-66
18	101.5	42.6	311	4	US-09-722-487-66
19	101.5	42.6	311	4	US-09-722-708-66
20	101	42.4	79	1	US-08-487-359-1
21	101	42.4	79	1	US-08-487-359-3
22	101	42.4	79	1	US-08-487-359-8
23	101	42.4	79	1	US-08-222-798A-1
24	101	42.4	79	1	US-08-222-798A-3
25	101	42.4	79	1	US-08-222-798A-8
26	98.5	41.4	42	4	US-09-030-619-162
27	98.5	41.4	79	1	US-08-487-359-2

28	98.5	41.4	79	1	US-08-487-359-4
29	98.5	41.4	79	1	US-08-222-798A-2
30	98.5	41.4	79	1	US-08-222-798A-4
31	96	40.3	16	3	US-09-024-975-3
32	96	40.3	16	4	US-08-930-777A-5
33	96	40.3	76	4	US-09-547-693-233
34	95	39.9	78	1	US-08-487-359-7
35	95	39.9	78	1	US-08-222-798A-7
36	94.5	39.7	424	4	US-09-949-016-7950
37	94	39.5	43	3	US-09-024-975-7
38	94	39.5	43	5	PCT-US95-12080-2
39	94	39.5	79	1	US-08-487-359-6
40	94	39.5	79	1	US-08-222-798A-6
41	94	39.5	176	4	US-09-917-340-28
42	94	39.5	288	4	US-09-270-767-42632
43	93	39.1	59	4	US-09-030-619-163
44	92.5	38.9	498	4	US-09-949-016-7108
45	92	38.7	15	4	US-08-930-777A-6

ALIGNMENTS

RESULT 1
US-08-162-052-1
; Sequence 1, Application US/08162052
; Patent No. 5489575
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong-Youn
; APPLICANT: BOMAN, Hans G
; APPLICANT: MUTT, Viktor
; APPLICANT: JORNWALL, Hans
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,052
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9101838-2
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92-22578
; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 003300-299
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-162-052-1

Query Match 100.0%; Score 238; DB 1; Length 39;

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Best Local Similarity 100.0%; Pred. No. 4.6e-17; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0;

Qy 1 RRRPPPPYLPRLPPPPPPPPRLPPRIPGFPFPPPPRFP 39
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Db 1 RRRPPPPYLPRLPPPPPPPPRLPPRIPGFPFPPPPRFP 39

RESULT 2
US-08-310-722-1
; Sequence 1, Application US/08310722
; Patent No. 5654273
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,722
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: CMC379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Boman, Hans G.
; AUTHORS: Mutt, Viktor
; AUTHORS: Jorvall, Hans
; TITLE: No. 5654273el Polypeptides And Their Use
; JOURNAL: PCT WO 92/25578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-310-722-1

Query Match 100.0%; Score 238; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.6e-17;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPPPYLPRLPPPPPPPPRLPPRIPGFPFPPPPRFP 39
    |||||
Db 1 RRRPPPPYLPRLPPPPPPPPRLPPRIPGFPFPPPPRFP 39

RESULT 3
US-08-419-066-1
; Sequence 1, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-1

Query Match 100.0%; Score 238; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.6e-17;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPPPYLPRLPPPPPPPPRLPPRIPGFPFPPPPRFP 39
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Db 1 RRRPPPPYLPRLPPPPPPPPRLPPRIPGFPFPPPPRFP 39

RESULT 4
US-08-728-333-1
; Sequence 1, Application US/08728333
; Patent No. 5863897
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,333
; FILING DATE:
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,722
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: CMCC379
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Boman, Hans G.
; AUTHORS: Mutt, Viktor
; AUTHORS: Jorvall, Hans
; TITLE: No. 5863897el Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-728-333-1

Query Match 100.0%; Score 238; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.6e-17;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RRRPPYLPRLPPPPPPPPPPRLPPRIIPGPPPPPPPP 39

RESULT 5
US-09-024-975-1
; Sequence 1, Application US/09024975
; Patent No. 6132233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:

Query Match 100.0%; Score 238; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.6e-17;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RRRPPYLPRLPPPPPPPPPPRLPPRIIPGPPPPPPPP 39

RESULT 6
US-08-930-777A-1
; Sequence 1, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; MOLECULE TYPE: peptide
US-08-930-777A-1

Query Match 100.0%; Score 238; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.6e-17;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPYLPRLPPPPPPPPPPRLPPRIIPGPPPPPPPP 39
Db 1 RRRPPYLPRLPPPPPPPPPPRLPPRIIPGPPPPPPPP 39

RESULT 7
US-08-930-777A-1
; Sequence 1, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; MOLECULE TYPE: peptide
US-08-930-777A-1

Query Match 100.0%; Score 238; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.6e-17;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPYLPRLPPPPPPPPPPRLPPRIIPGPPPPPPPP 39
Db 1 RRRPPYLPRLPPPPPPPPPPRLPPRIIPGPPPPPPPP 39
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RESULT 8
US-09-739-535-1
; Sequence 1, Application US/09739535
; Patent No. 6794490
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/739,535
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRI
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-739-535-1

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RESULT 10
US-09-024-975-2
; Sequence 2, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/802,306
FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25585-A
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-975-2

Query Match 65.1%; Score 155; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RRRPPYLPRLPPPPPPPPRLPPRI 26

RESULT 11
US-08-930-777A-2
Sequence 2, Application US/08930777A
Patent No. 6713605
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996

ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-930-777A-2

Query Match 65.1%; Score 155; DB 4; Length 26;
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
US-08-930-777A-3
Sequence 3, Application US/08930777A
Patent No. 6713605
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-930-777A-3

Query Match 58.8%; Score 140; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.4e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PRPPYLPRLPPPPPPPPRLPPRI 26

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Db      1 PPPYLPRLPPPPPPPPPPPPRI 23
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RESULT 13
US-08-930-777A-4
; Sequence 4, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-930-777A-4

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Db      1 RRRPPYLPRLPPPPFP 19
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RESULT 14
US-08-487-359-5
; Sequence 5, Application US/08487359
; Patent No. 563229
; GENERAL INFORMATION:
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: LEHRER, ROBERT I.
; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington, D.C.
; STATE: CA
; COUNTRY: USA

Query Match      44.5%; Score 106; DB 1; Length 78;
Best Local Similarity 63.4%; Pred. No. 0.00058;
Matches 26; Conservative 0; Mismatches 7; Indels 8; Gaps 5;

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Db      10 PRFPFPQPPGRFPFPNPPGPRFP---PPQFPGRFPFPFP 47
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RESULT 15
US-08-222-798A-5
; Sequence 5, Application US/08222798A
; Patent No. 5804553
; GENERAL INFORMATION:
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: LEHRER, ROBERT I.
; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington, D.C.
; STATE: CA
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,798A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0553.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-0763
; TELEFAX: (202) 887-0763
; TELETYPE: 90-4030
; INFORMATION FOR SEQ ID NO: 5:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-222-798A-5

Query Match 44.5%; Score 106; DB 1; Length 78;
Best Local Similarity 63.4%; Pred. No. 0.00058;
Matches 26; Conservative 0; Mismatches 7; Indels 8; Gaps 5;

QY 4 PR--PPYLPRLPRP-PPPPFP-PRLPPRLPPGFP-PPPPPPFP 39
Db 10 PRPPPPQFPGRPPPPNPPGPRFP---PPQFGRPPPPFP 47

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:05:05 ; Search time 143.945 Seconds
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Title: US-10-014-147-1

Perfect score: 238

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	238	100.0	39	15	US-10-391-155-2
4	238	100.0	39	15	US-10-391-155-6
5	238	100.0	39	15	US-10-651-147-1
6	238	100.0	42	16	US-10-344-709C-18
7	238	100.0	42	17	US-10-916-185-14
8	238	100.0	42	18	US-10-991-286A-44
9	238	100.0	42	20	US-11-004-379-20
10	221.5	93.1	38	9	US-09-738-742-1
11	221.5	93.1	38	9	US-09-739-535-1

12	155	65.1	26	14	US-10-014-147-2	Sequence 2, Appli
13	155	65.1	26	15	US-10-651-147-2	Sequence 3, Appli
14	140	58.8	23	14	US-10-014-147-3	Sequence 2, Appli
15	140	58.8	23	15	US-10-651-147-3	Sequence 3, Appli
16	119.5	50.2	483	16	US-10-437-963-191498	Sequence 131498
17	119	50.0	91	16	US-10-425-115-200180	Sequence 200180
18	118	49.6	83	16	US-10-437-963-118176	Sequence 118176
19	118	49.6	333	16	US-10-437-963-191891	Sequence 191891
20	116	48.7	19	14	US-10-014-147-4	Sequence 4, Appli
21	116	48.7	19	15	US-10-651-147-4	Sequence 132896
22	116	48.7	276	16	US-10-437-963-132896	Sequence 132896
23	114	47.9	200	16	US-10-425-115-206766	Sequence 206766
24	114	47.9	245	16	US-10-425-115-206869	Sequence 206869
25	111	46.6	159	16	US-10-425-115-320315	Sequence 320315
26	111	46.6	323	16	US-10-437-963-175653	Sequence 175653
27	111	46.6	431	16	US-10-437-963-204963	Sequence 204963
28	110.5	46.4	96	16	US-10-437-963-120965	Sequence 120965
29	110.5	46.4	204	16	US-10-437-963-180133	Sequence 180133
30	109	45.8	173	16	US-10-437-963-191890	Sequence 191890
31	108	45.4	91	16	US-10-437-963-160130	Sequence 160130
32	108	45.4	136	16	US-10-425-115-222187	Sequence 222187
33	107	45.0	270	16	US-10-437-963-197222	Sequence 197222
34	107	45.0	322	16	US-10-425-115-316075	Sequence 316075
35	106	44.5	151	16	US-10-437-963-134683	Sequence 134683
36	106	44.5	153	15	US-10-425-114-53570	Sequence 53570, A
37	106	44.5	321	16	US-10-425-115-202316	Sequence 202316
38	106	44.5	329	16	US-10-437-963-163296	Sequence 163296
39	106	44.5	621	16	US-10-437-963-177697	Sequence 177697
40	105.5	44.3	215	16	US-10-767-701-35371	Sequence 35371, A
41	105.5	44.3	224	16	US-10-425-115-289952	Sequence 289952
42	105	44.1	87	14	US-10-029-386-30727	Sequence 30727, A
43	105	44.1	156	15	US-10-424-599-144804	Sequence 144804
44	105	44.1	180	15	US-10-424-599-242969	Sequence 242969
45	104.5	43.9	76	16	US-10-425-115-236218	Sequence 236218

ALIGNMENTS

RESULT 1

US-10-014-147-1
; Sequence 1, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-014-147-1
Query Match 100.0%; Score 238; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.1e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRRPPPPYLRPPPPPPPPPPRLPPRIPPGFPPPPPPRFP 39
Db 1 RRRPPPPYLRPPPPPPPPPPRLPPRIPPGFPPPPPPRFP 39
RESULT 2
US-10-391-155-1
; Sequence 1, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated
; selective inhibition of IKBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: WordPerfect version 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-044/D
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-391-155-1
Query Match 100.0%; Score 238; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.1e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRRPPPPYLRPPPPPPPPPPRLPPRIPPGFPPPPPPRFP 39
Db 1 RRRPPPPYLRPPPPPPPPPPRLPPRIPPGFPPPPPPRFP 39
RESULT 3
US-10-391-155-2
; Sequence 2, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated
; selective inhibition of IKBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: WordPerfect version 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-044/D
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-391-155-2
Query Match 100.0%; Score 238; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.1e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRRPPPPYLRPPPPPPPPPPRLPPRIPPGFPPPPPPRFP 39
Db 1 RRRPPPPYLRPPPPPPPPPPRLPPRIPPGFPPPPPPRFP 39
RESULT 4
US-10-391-155-6
; Sequence 6, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated
; selective inhibition of IKBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: WordPerfect version 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-044/D
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-391-155-6
Query Match 100.0%; Score 238; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.1e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRRPPPPYLRPPPPPPPPPPRLPPRIPPGFPPPPPPRFP 39
Db 1 RRRPPPPYLRPPPPPPPPPPRLPPRIPPGFPPPPPPRFP 39

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APPLICATION NUMBER: US/10/391,155
FILING DATE: 18-Mar-2003
CLASSIFICATION: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCES/DOCKET NUMBER: BIS-044/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-391-155-6

Query Match 100.0%; Score 238; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.1e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPYLPRLPPPPPPPPPPRLPPRIIPGPPPPPPPP 39
|||||
DB 1 RRRPPYLPRLPPPPPPPPPPRLPPRIIPGPPPPPPPP 39
|||||

RESULT 5
US-10-651-147-1
Sequence 1, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/651,147
FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCES/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-651-147-1

Query Match 100.0%; Score 238; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.1e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPYLPRLPPPPPPPPPPRLPPRIIPGPPPPPPPP 39
|||||
DB 1 RRRPPYLPRLPPPPPPPPPPRLPPRIIPGPPPPPPPP 39
|||||

RESULT 6
US-10-344-709C-18
Sequence 18, Application US/10344709C
Publication No. US20040170642A1
GENERAL INFORMATION:
APPLICANT: JORG FRITZ ET AL.
TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
FILE REFERENCE: SONN:030US
CURRENT APPLICATION NUMBER: US/10/344,709C
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: PCT/EP01/09529
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: A 1416/2000
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 42
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-18

Query Match 100.0%; Score 238; DB 16; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.6e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPYLPRLPPPPPPPPPPRLPPRIIPGPPPPPPPP 39
|||||
DB 1 RRRPPYLPRLPPPPPPPPPPRLPPRIIPGPPPPPPPP 39
|||||

RESULT 7
US-10-916-185-14
Sequence 14, Application US/10916185
Publication No. US20050107325A1
GENERAL INFORMATION:
APPLICANT: Manoharan, Muthiah
APPLICANT: Kesavan, Venkatasamy
APPLICANT: Rajeev, Kallanthottathil G.
TITLE OF INVENTION: MODIFIED IRNA AGENTS
FILE REFERENCE: 14174-091001
CURRENT APPLICATION NUMBER: US/10/916,185
CURRENT FILING DATE: 2004-08-10
PRIOR APPLICATION NUMBER: PCT/US2004/011829
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/465,665
PRIOR FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/463,772
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US 60/469,612
PRIOR FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 60/465,802
PRIOR FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/493,986
PRIOR FILING DATE: 2003-08-08
PRIOR APPLICATION NUMBER: US 60/494,597
PRIOR FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US 60/503,414
PRIOR FILING DATE: 2003-09-15
PRIOR APPLICATION NUMBER: US 60/506,341

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; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 60/510,246
; PRIOR FILING DATE: 2003-10-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptides
US-10-916-185-14

Query Match      100.0%; Score 238; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.6e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPVLPRLPRPPPPPPRLPPRIIPGFPFRPPRP 39
| | | | | | | | | | | | | | | | | | | | | |
DB 1 RRRPPVLPRLPRPPPPPPPPRLPPRIIPGFPFRPPRP 39
| | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-10-991-286A-44
; Sequence 44, Application US/10991286A
; Publication No. US20050186591A1
; GENERAL INFORMATION:
; APPLICANT: Bumcrot, David
; APPLICANT: Farrer, Matthew J.
; APPLICANT: Maraganore, Demetrius M.
; APPLICANT: Voynlocher, Hans-Peter
; TITLE OF INVENTION: METHOD OF TREATING NEURODEGENERATIVE DISEASE
; FILE REFERENCE: 17574-003001
; CURRENT APPLICATION NUMBER: US/10/991,286A
; CURRENT FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: PCT/US2004/18271
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/476,947
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptide
US-10-991-286A-44

Query Match      100.0%; Score 238; DB 18; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.6e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPVLPRLPRPPPPPPPPRLPPRIIPGFPFRPPRP 39
| | | | | | | | | | | | | | | | | | | | | |
DB 1 RRRPPVLPRLPRPPPPPPPPRLPPRIIPGFPFRPPRP 39
| | | | | | | | | | | | | | | | | | | | | |

RESULT 9
US-11-004-379-20
; Sequence 20, Application US/11004379
; Publication No. US2005015337A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: iRNA CONJUGATES
; FILE REFERENCE: 14174-067001
; CURRENT APPLICATION NUMBER: US/11/004,379
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: PCT/US04/10586
; PRIOR FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 60/460,783
; PRIOR FILING DATE: 2003-04-03

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; PRIOR APPLICATION NUMBER: US 60/462,894
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptides
US-11-004-379-20

Query Match      100.0%; Score 238; DB 20; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.6e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPVLPRLPRPPPPPPPPRLPPRIIPGFPFRPPRP 39
| | | | | | | | | | | | | | | | | | | | | |
DB 1 RRRPPVLPRLPRPPPPPPPPRLPPRIIPGFPFRPPRP 39
| | | | | | | | | | | | | | | | | | | | | |

RESULT 10
US-09-738-742-1
; Sequence 1, Application US/09738742
; Publication No. US20020025924A1
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/738,742
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-738-742-1

Query Match      93.1%; Score 221.5; DB 9; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.1e-12;
Matches 38; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 RRRPPVLPRLPRPPPPPPPPRLPPRIIPGFPFRPPRP 39
| | | | | | | | | | | | | | | | | | | | | |
DB 1 RRRPPVLPRLPRPPPPPPPPRLPPRIIPGFPFRPPRP 38
| | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-09-739-535-1
; Sequence 1, Application US/09739535
; Publication No. US20020058785A1
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060

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1 RRRPRPPYLPRPPPPPPPPRLPPRI 26

Db

US-10-651-147-2

Query Match 93.1%; Score 221.5; DB 9; Length 38;

Best Local Similarity 97.4%; Pred. No. 2.1e-12; Indels 1; Gaps 1;

Matches 38; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 RRRPRPPYLPRPPPPPPPPRLPPRI 39

Db

1 RRRPRPPYLPRPPPPPPPPRLPPRI 38

RESULT 12

US-10-014-147-2

Sequence 2, Application US/10014147

Publication No. US20030125249A1

GENERAL INFORMATION:

APPLICANT: Blecha, Frank

TITLE OF INVENTION: Synthetic Antimicrobial Peptide

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hovey, Williams, Timmons & Collins

STREET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City

STATE: Missouri

COUNTRY: U.S.A.

ZIP: 64108

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/014,147

FILING DATE: 07-Dec-2001

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/930,777A

FILING DATE: October 8, 1997

APPLICATION NUMBER: PCT/US96/04674

FILING DATE: April 10, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Collins, John M.

REGISTRATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 23625-A

TELEPHONE: (816) 474-9050

TELEFAX: (816) 474-9057

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-014-147-2

Query Match 65.1%; Score 155; DB 14; Length 26;

Best Local Similarity 100.0%; Pred. No. 7.4e-07;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RRRPRPPYLPRPPPPPPPPRLPPRI 26

Db

1 RRRPRPPYLPRPPPPPPPPRLPPRI 26

RESULT 14

US-10-014-147-3

Sequence 3, Application US/10014147

Publication No. US20030125249A1

GENERAL INFORMATION:

APPLICANT: Blecha, Frank

TITLE OF INVENTION: Synthetic Antimicrobial Peptide

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hovey, Williams, Timmons & Collins

STREET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City

STATE: Missouri

COUNTRY: U.S.A.

ZIP: 64108

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/014,147

FILING DATE: 07-Dec-2001

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/930,777A

FILING DATE: October 8, 1997

APPLICATION NUMBER: PCT/US96/04674

FILING DATE: April 10, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Collins, John M.

REGISTRATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 23625-A

TELEPHONE: (816) 474-9050

TELEFAX: (816) 474-9057

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-014-147-2

Query Match 65.1%; Score 155; DB 14; Length 26;

Best Local Similarity 100.0%; Pred. No. 7.4e-07;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RRRPRPPYLPRPPPPPPPPRLPPRI 26

Db

1 RRRPRPPYLPRPPPPPPPPRLPPRI 26

1 RRRPRPPYLPRPPPPPPPPRLPPRI 26

Db

US-10-651-147-2

Query Match 65.1%; Score 155; DB 15; Length 26;

Best Local Similarity 100.0%; Pred. No. 7.4e-07;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RRRPRPPYLPRPPPPPPPPRLPPRI 26

Db

1 RRRPRPPYLPRPPPPPPPPRLPPRI 26

RESULT 13

US-10-651-147-2

Sequence 2, Application US/10651147

Publication No. US20040043934A1

GENERAL INFORMATION:

APPLICANT: Blecha, Frank

TITLE OF INVENTION: Synthetic Antimicrobial Peptide

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hovey, Williams, Timmons & Collins

STREET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City

STATE: Missouri

COUNTRY: U.S.A.

ZIP: 64108

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/651,147

FILING DATE: 28-Aug-2003

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/930,777A

FILING DATE: October 8, 1997

APPLICATION NUMBER: PCT/US96/04674

FILING DATE: April 10, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Collins, John M.

REGISTRATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 23625-A

TELEPHONE: (816) 474-9050

TELEFAX: (816) 474-9057

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-651-147-2

Query Match 65.1%; Score 155; DB 15; Length 26;

Best Local Similarity 100.0%; Pred. No. 7.4e-07;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RRRPRPPYLPRPPPPPPPPRLPPRI 26

Db

1 RRRPRPPYLPRPPPPPPPPRLPPRI 26

RESULT 14

US-10-014-147-3

Sequence 3, Application US/10014147

Publication No. US20030125249A1

GENERAL INFORMATION:

APPLICANT: Blecha, Frank

TITLE OF INVENTION: Synthetic Antimicrobial Peptide

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hovey, Williams, Timmons & Collins

STREET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City

STATE: Missouri

COUNTRY: U.S.A.

ZIP: 64108

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/651,147

FILING DATE: 28-Aug-2003

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/930,777A

FILING DATE: October 8, 1997

APPLICATION NUMBER: PCT/US96/04674

FILING DATE: April 10, 1996

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NAME: Collins, John M.

REGISTRATION NUMBER: 26,262

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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-651-147-2

Query Match 65.1%; Score 155; DB 15; Length 26;

Best Local Similarity 100.0%; Pred. No. 7.4e-07;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RRRPRPPYLPRPPPPPPPPRLPPRI 26

Db

1 RRRPRPPYLPRPPPPPPPPRLPPRI 26

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/10/014,147
; APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-014-147-3

Query Match 58.8%; Score 140; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PRPPYLPRPPPPPPRLPPRI 26
DB 1 PRPPYLPRPPPPPPPPRLPPRI 23

RESULT 15
US-10-651-147-3
; Sequence 3, Application US/10651147
; Publication No. US2004004394A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/651,147
; FILING DATE: 28-Aug-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
```

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;
;
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-651-147-3

Query Match 58.8%; Score 140; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PRPPYLPRPPPPPPRLPPRI 26
DB 1 PRPPYLPRPPPPPPPPRLPPRI 23

Search completed: October 26, 2005, 05:28:55
Job time : 152.945 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:51:43 ; Search time 102.345 Seconds
(without alignments)
98.253 Million cell updates/sec

Title: US-10-014-147-2

Perfect score: 155
Sequence: 1 RRRRRPPVLP RRRPPPPPPPPRLPPRI 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155	100.0	26	AAW01447	Leukocyte
2	155	100.0	26	AAW75723	Proline-a
3	155	100.0	26	ADL67257	Antimicro
4	155	100.0	26	ADL67255	Antimicro
5	155	100.0	39	AAR30491	Antibacte
6	155	100.0	39	AAR99121	Magainin-
7	155	100.0	39	AAR94446	Synducin
8	155	100.0	39	AAW01446	Leukocyte
9	155	100.0	39	AAW75722	Proline-a
10	155	100.0	39	AAB36888	PR-39 pep
11	155	100.0	39	AAB97280	PR-39 pep
12	155	100.0	39	AAB84690	Amino aci
13	155	100.0	39	ADD35364	Antimicro
14	155	100.0	39	ADL67254	Proline-a
15	155	100.0	39	ADL67254	Antimicro
16	155	100.0	42	ABD07714	Antimicro
17	155	100.0	42	ADR82250	Cell perm
18	155	100.0	42	AAB51194	E. coli A
19	140	90.3	23	AAW01451	Leukocyte
20	140	90.3	23	ADL67256	Proline-a
21	140	90.3	23	ADL67256	Antimicro
22	116	74.8	19	AAW01452	Leukocyte
23	116	74.8	19	ADL67257	Proline-a
24	116	74.8	19	ADL67257	Antimicro
25	96	61.9	16	AAW01448	Leukocyte

26	96	61.9	16	2	AAW75724	Proline/A
27	96	61.9	16	8	ADL67258	Proline-a
28	96	61.9	16	8	ADL67258	Antimicro
29	90	58.1	15	3	AAB26885	PR-39 der
30	90	58.1	15	4	AAB97277	PR-39 der
31	90	58.1	15	4	AAB84691	Amino aci
32	83	53.5	14	2	AAW01450	Leukocyte
33	83	53.5	14	2	AAW75725	Proline/A
34	83	53.5	14	8	ADL67260	Proline-a
35	83	53.5	14	8	ADL67260	Antimicro
36	82	52.9	35	2	AAR79212	Bactenecl
37	82	52.9	59	2	AAW66400	Cationic
38	82	52.9	59	3	AAW91699	Cationic
39	82	52.9	59	6	ABU59576	Cationic
40	82	52.9	60	5	ABB07713	Antimicro
41	82	52.9	62	4	AAB51197	E. coli A
42	78	50.3	278	2	AAR79095	Rat Fas 1
43	78	50.3	278	2	AAW98069	Rat Fas 1
44	78	50.3	278	2	AAW95040	Rat FasL
45	78	50.3	278	5	AAO19029	Human Fas

ALIGNMENTS

RESULT 1

AAW01447
ID AAW01447 standard; peptide; 26 AA.

XX AAW01447;

XX 18-JUN-1997 (first entry)

XX Leukocyte O2- production inhibitor peptide PR26.

DE Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
KW DNA synthesis; protein synthesis; inhibitor; syndecin expression;
KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
KW tissue damage; oxygen radical; inflammatory disease; therapy.

XX Synthetic.

XX WO9632129-A1.

XX 17-OCT-1996.

XX 10-APR-1996; 96WO-US004674.

XX 10-APR-1995; 95US-00419066.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Blecha F, Shi J;

XX WPI; 1996-476842/47.

XX Inhibition of leukocyte superoxide anion prodn. and attraction of
leukocytes - using peptide(s) partic. based on antimicrobial PR-39.

XX Claim 3; Page 26; 45pp; English.

XX AAW01447-W01454 represent fragments of the proline-arginine rich
antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
isolated from porcine small intestine, and has also been identified in
human and porcine neutrophils. PR39 kills bacteria by interfering with
DNA and/or protein synthesis. PR39 also induces syndecin expression on
mesenchymal cells. Syndecins are important in wound repair, showing that
PR39 can be used in wound repair, as well as in antibacterial agents.
These sequences, and PR39, can be used in the method of the invention.
The method of the invention is for inhibiting leukocyte superoxide anion
(O2-) production. The method comprises administering to a leukocyte a
peptide (such as this sequence) capable of inhibiting leukocyte O2-

CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting tissue
 CC damage at the wound site caused by excessive oxygen radicals produced by
 CC these leukocytes. They can also be used to develop products for treating
 CC inflammatory disease states
 XX
 SQ Sequence 26 AA;

Query Match 100.0%; Score 155; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.1e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRRPRPPVLP RRRPPPPPPPPRLPPRI 26
 |||||
 Db 1 RRRPRPPVLP RRRPPPPPPPPRLPPRI 26
 |||||

RESULT 2
 AAW75723
 ID AAW75723 standard; peptide; 26 AA.
 XX
 AC AAW75723;

DT 19-NOV-1998 (first entry)
 DE Proline/Arginine rich peptide PR-26.
 XX

Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;
 KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;
 KW coronary bypass; organ transplantation surgery.
 XX

OS Synthetic.
 XX
 PN WO9835690-A1.
 XX

PD 20-AUG-1998.
 PF 17-FEB-1998; 98WO-US003207.
 XX

PR 18-FEB-1997; 97US-00802306.
 PR 16-FEB-1998; 98US-00024975.
 XX

PA (UNIV) UNIV KANSAS STATE RES FOUND.
 XX
 PI Ross CR, Blecha F, Shi J;
 XX

DR WPI; 1998-495359/42.
 XX
 PT Reduction of reperfusion injury in temporarily occluded blood vessels -
 PT by administration of a peptide which is rich in proline or arginine
 PT residues.

PS Claim 3; Page 14-15; 35pp; English.
 XX

XX Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
 CC administration into a mammal's bloodstream reduce reperfusion injury
 CC (production of reactive oxygen species, neutrophil adherence to
 CC endothelium, and extravasation of neutrophils). These peptides have two
 CC requirements: they contain the consensus sequence PXXP, where P is a
 CC proline residue and X is any amino acid residue, which has been found to
 CC inhibit superoxide production, and secondly they have arginine residues
 CC adjacent to these motifs, required for effective inhibition. It was
 CC established by structural and function analysis that a peptide should
 CC ideally contain 4 or 6 of these motifs, and that inhibitory activity is
 CC correlated with the increase of length of peptides. The effectiveness of
 CC these peptides was determined by investigating the production of the
 CC neutrophil superoxide anion, and also the inhibition of neutrophil
 CC chemotaxis. From this, it was found that all of the peptides inhibited
 CC NADPH oxidase to some extent. All of the peptides also inhibit neutrophil
 CC down regulator of NADPH oxidase yet discovered, and from the data
 CC produced, it can be suggested to be involved in eliminating or reducing
 CC the reperfusion injury induced adhesion and extraction of neutrophils.

CC The peptides are also useful in connection with surgical procedures such
 CC as coronary bypass and organ transplantation surgery
 XX
 SQ Sequence 26 AA;

Query Match 100.0%; Score 155; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.1e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRRPRPPVLP RRRPPPPPPPPRLPPRI 26
 |||||
 Db 1 RRRPRPPVLP RRRPPPPPPPPRLPPRI 26
 |||||

RESULT 3
 ADE86113
 ID ADE86113 standard; peptide; 26 AA.
 XX
 AC ADE86113;

DT 29-JAN-2004 (first entry)
 DE Proline-arginine (PR)-rich antimicrobial peptide PR-26.
 XX

Leukocyte superoxide anion; leukocyte O2- production;
 KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;
 KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;
 KW tissue damage; oxygen radical; antibacterial.
 XX

OS Synthetic.
 XX
 PN US2003125249-A1.
 XX

PD 03-JUL-2003.
 PF 07-DEC-2001; 2001US-00014147.
 XX

PR 10-APR-1995; 95US-00419066.
 PR 08-OCT-1997; 97US-00930777.
 XX

PA (BLEC/) BLECHA F.
 PA (SHIJ/) SHI J.
 XX

PI Blecha F, Shi J;
 XX
 DR WPI; 2004-059188/06.
 XX

PT Attracting leukocyte to location by administering peptide including
 PT proline-arginine-rich antimicrobial peptide or its truncated analogs to
 PT the location.

PS Claim 3; SEQ ID NO 2; 24pp; English.
 XX

XX The present invention relates to a method of inhibiting leukocyte
 CC superoxide anion (O2-) production and/or attracting leukocytes. The
 CC method comprises the use of proline-arginine (PR)-rich antimicrobial
 CC peptides or their truncated analogues. The method is useful for
 CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or
 CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are
 CC useful as medicaments to fight infection by attracting leukocytes to a
 CC wound site, while restricting tissue damage at the wound site caused by
 CC excessive oxygen radicals produced by these leukocytes. The present
 CC sequence represents a PR-rich antimicrobial peptide.

XX
 SQ Sequence 26 AA;
 Query Match 100.0%; Score 155; DB 8; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.1e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPVLP RRRPPPPPPPPRLPPRI 26
 |||||
 Db 1 RRRPRPPVLP RRRPPPPPPPPRLPPRI 26
 |||||

Query Match 100.0%; Score 155; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;

KW STD; sexually transmitted disease; HIV; human immunodeficiency virus;
 KW herpes simplex virus; HSV; Neisseria gonorrhoeae; Candida; Chlamydia;
 KW magainin; antimicrobial; squalamine.

XX Synthetic.

XX Key Location/Qualifiers
 FH 39
 FT Modified-site /note= "amidated"

XX W09608270-A2.

XX 21-MAR-1996.

XX 13-SEP-1995; 95WO-US011675.

XX 13-SEP-1994; 94US-00305475.

XX (MAGA-) MAGAININ PHARM INC.

XX Jacob L, Zasloff M, Williams T, Bedi G;

XX WPI; 1996-179725/18.

XX Inhibiting sexually transmitted disease e.g. HIV or herpes simplex - by
 PT administering magainin antimicrobial or squalamine cpd. to inhibit
 PT transmission.

XX Example 1; Page 32; 60pp; English.

XX AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may be
 CC used to treat sexually transmitted diseases (STDs) caused by Chlamydia,
 CC HIV, herpes simplex virus, Neisseria gonorrhoeae or Candida infection.
 CC The peptides inhibit STDs by either killing the infectious organism,
 CC impeding the infection mechanism or interrupting the replication cycle of
 CC the organism. Squalamine (an aninosterol host defence molecule of the dog
 CC fish shark Squalus acanthias) and PGla (a frog antimicrobial peptide)
 CC analogues may also be useful in inhibiting STD infection and transmission

XX Sequence 39 AA;

Query Match 100.0%; Score 155; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 7.2e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRPRPPVLPRLPPPPPPPPRLPPRI 26

Db 1 RRRPRPPVLPRLPPPPPPPPRLPPRI 26

RESULT 7

AAR94446

ID AAR94446 standard; peptide; 39 AA.

XX AAR94446;

XX 05-NOV-1996 (first entry)

DE Synducin peptide (PR-39) induces syndecan expression.

XX Synducin; induction; expression; syndecan-1; syndecan-4; surface;
 KW mesenchymal cell; fibroblast; epithelial; PR-39; treatment; stasis;
 KW decubitus; ulcers; keloids; skin burns; ischemic tissues;
 KW hypercoagulation states; prevention; tumour metastasis; restenosis;
 KW inhibition; angiogenesis; proliferation; endothelial.

XX Synthetic.

XX W09609322-A2.

XX 28-MAR-1996.

XX 22-SEP-1995; 95WO-US012080.

XX 22-SEP-1994; 94US-00310722.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX Gallo RL, Bernfield M;
 XX WPI; 1996-188401/19.
 XX Modulating mesenchymal interaction by administration of synducin - used
 PT in the treatment of wounds, tumours, restenosis, etc.
 XX Claim 4; Page 26; 34pp; English.

XX The present peptide is a synducin, which induces the expression of
 CC syndecan-1 and syndecan-4 on the surface of mesenchymal cells, esp.
 CC fibroblasts and epithelial cells. The 36 N-terminal amino acids of the
 CC peptide were found to be identical to the 36 N-terminal amino acids of PR
 CC -39, a pro and Arg rich antibacterial peptide previously found in porcine
 CC intestine (W09222578). Synducins may be used in the treatment of stasis
 CC and decubitus ulcers, keloids, skin burns, ischemic tissues and
 CC hypercoagulation states, prevention of tumour metastasis, restenosis
 CC inhibition and endothelial cell angiogenesis and proliferation induction.
 CC Human microvascular endothelial cells were assayed for syndecan-4
 CC expression following exposure to 5 μ g wound fluid, dbcAMP (1 mM), the
 CC present peptide (10 microm) or a blank, to give respective cell surface
 CC syndecan-4 values (mOD/m in) of approx. 1.75, 1.70, 1.80 and 0.95

XX Sequence 39 AA;

Query Match 100.0%; Score 155; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 7.2e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRPRPPVLPRLPPPPPPPPRLPPRI 26

Db 1 RRRPRPPVLPRLPPPPPPPPRLPPRI 26

RESULT 8

AAW01446

ID AAW01446 standard; peptide; 39 AA.

XX AAW01446;

XX 18-JUN-1997 (first entry)

DE Leukocyte O2- production inhibitor peptide PR39.

XX Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
 KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 KW tissue damage; oxygen radical; inflammatory disease; therapy.

XX Synthetic.

XX W09632129-A1.

XX 17-OCT-1996.

XX 10-APR-1996; 96WO-US004674.

XX 10-APR-1995; 95US-00419066.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Blecha F, Shi J;

XX WPI; 1996-476842/47.

XX Inhibition of leukocyte super:oxide anion prodn. and attraction of
 PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.

XX PS Claim 2; Page 26; 45pp; English.

XX CC This sequence represents the proline-arginine rich antimicrobial peptide

CC CC PR39. The PR39 sequence was first isolated from porcine small intestine,

CC CC and has also been identified in human and porcine neutrophils. PR39 kills

CC CC bacteria by interfering with DNA and/or protein synthesis. PR39 also

CC CC induces syndecan expression on mesenchymal cells. Syndecans are important

CC CC in wound repair, showing that PR39 can be used in wound repair, as well

CC CC as in antibacterial agents. This sequence, and the fragments of it shown

CC CC in AA01447-W01454, can be used in the method of the invention. The

CC CC method of the invention is for inhibiting leukocyte superoxide anion (O2-

CC CC) production. The method comprises administering to a leukocyte a peptide

CC CC (such as this sequence) capable of inhibiting leukocyte O2- production.

CC CC The peptides can be used as medicaments for fighting infection by

CC CC attracting leukocytes to a wound site and restricting tissue damage at

CC CC the wound site caused by excessive oxygen radicals produced by these

CC CC leukocytes. They can also be used to develop products for treating

CC CC inflammatory disease states

XX CC Sequence 39 AA;

XX CC

Query Match 100.0%; Score 155; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 7.2e-09;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RRRPPPPFPFPPRLPPRI 26

DB 1 RRRPRPPYLP RRRPPPPFPFPPRLPPRI 26

RESULT 9

AAW75722

ID AAW75722 standard; peptide; 39 AA.

XX AC AAW75722;

XX DT 19-NOV-1998 (first entry)

XX DE Proline/Arginine rich peptide PR-39.

XX KW Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;

XX KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;

XX KW coronary bypass; organ transplantation surgery.

XX OS Synthetic.

XX PN W09835690-A1.

XX PD 20-AUG-1998.

XX PF 17-FEB-1998; 98WO-US003207.

XX PR 18-FEB-1997; 97US-00802306.

XX PR 16-FEB-1998; 98US-00024975.

XX PA (UNIV) UNIV KANSAS STATE RES FOUND.

XX PI Ross CR, Blecha F, Shi J;

XX PI WPI; 1998-495359/42.

XX PT Reduction of reperfusion injury in temporarily occluded blood vessels -

XX PT by administration of a peptide which is rich in proline or arginine

XX PT residues.

XX PS Claim 3; Page 14; 35pp; English.

XX CC Sequences AAW75722-W75732 are proline/arginine rich peptides that upon

CC CC administration into a mammal's bloodstream reduce reperfusion injury

CC CC (production of reactive oxygen species, neutrophil adherence to

CC CC endothelium, and extravasation of neutrophils). These peptides have two

CC CC requirements: they contain the consensus sequence PXXP, where P is a

CC proline residue and X is any amino acid residue, which has been found to

CC inhibit superoxide production, and secondly they have arginine residues

CC adjacent to these motifs, required for effective inhibition. It was

CC established by structural and function analysis that a peptide should

CC ideally contain 4 or 6 of these motifs, and that inhibitory activity is

CC correlated with the increase of length of peptides. The effectiveness of

CC these peptides was determined by investigating the production of the

CC neutrophil superoxide anion, and also the inhibition of neutrophil

CC chemotaxis. From this, it was found that all of the peptides inhibited

CC NADPH oxidase to some extent. All of the peptides also inhibit neutrophil

CC oxidase activity. PR-39 is believed, to be the most potent endogenous

CC down regulator of NADPH oxidase yet discovered, and from the data

CC produced, it can be suggested to be involved in eliminating or reducing

CC the reperfusion injury induced adhesion and extraction of neutrophils.

CC The peptides are also useful in connection with surgical procedures such

CC as coronary bypass and organ transplantation surgery

XX CC Sequence 39 AA;

XX CC

Query Match 100.0%; Score 155; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 7.2e-09;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RRRPPPPFPFPPRLPPRI 26

DB 1 RRRPRPPYLP RRRPPPPFPFPPRLPPRI 26

RESULT 10

AAW75722

ID AAW75722 standard; peptide; 39 AA.

XX AC AAW75722;

XX DT 01-FEB-2001 (first entry)

XX DE PR-39 peptide used in angiogenesis control.

XX KW Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;

XX KW myocardial ischaemia; proteasome.

XX OS Synthetic.

XX PN W0200057895-A1.

XX PD 05-OCT-2000.

XX PF 16-MAR-2000; 2000WO-US007050.

XX PR 26-MAR-1999; 99US-00276868.

XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX PI Simons M, Gao Y;

XX PI WPI; 2000-628319/60.

XX PT Stimulating angiogenesis in situ, useful e.g. for treating anoxia and

XX PT infarction, by administering a PR-39 oligopeptide that regulates

XX PT enzymatic activity of proteasomes.

XX PS Disclosure; Page 21; 51pp; English.

XX CC This invention relates to a method for the stimulation of angiogenesis in

CC CC situ within a targeted collection of viable cells. The method comprises

CC CC introducing, into the cytoplasm, at least 1 member of the PR-39

CC CC oligopeptide collective, which interacts with cytoplasmic proteasomes.

CC CC Part of the proteolytic activity of the proteasomes is selectively

CC CC altered so as to stimulate angiogenesis. The method is used to induce

CC CC angiogenesis in tissue that has suffered anoxia or infarction, e.g.

CC CC myocardial infarction or chronic myocardial ischaemia, and also to study

CC CC the mechanisms that control angiogenesis. The present sequence represents

CC CC the PR-39 peptide from which peptide used in the method of the invention

CC are derived

XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 155; DB 3; Length 39;

Best Local Similarity	100.0%	Pred. No. 7.2e-09;
Matches 26;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 RRRPPPYLPRRPPPPFFPRLPPRI	26
D_b	1 RRRPPPYLPRRPPPPFFPRLPPRI	26

RESULT 11
AAB97280
ID AAB97280 standard; peptide; 39 AA.

AC AAB97280;

DT 09-AUG-2001 (first entry)

PR-39 peptide.

PR-39; cathelin; inflammation; wound healing; myocardial infarction;
KW proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;
KW anoxia; chronic myocardial ischaemia; heart tissue.

Unidentified.

AA PN WO200130368-A1.

03-MAY-2001.

06-OCT-2000: 2000WO-US027552.

PR 25-OCT-1999:

XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX

XX
DR WPI: 2001-355179/37.

Stimulation of angiogenesis and inhibition of proteasome mediated PT degradation in cells, by introduction of PR-39 oligopeptide or its N-terminal fragments or their conjugates, for use in anoxia and infarction PT conditions.

XX
PS
Disclosure: Page 21: 52pp: English.

Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39 is a member of the cathelin family of proteins, mature PR-39 represented by the present sequence is 39 amino acids in length, and has been shown to play a role in several inflammatory events including wound healing and myocardial infarction. The PR-39 derived family of oligopeptides cause selective inhibition of proteasome mediated degeneration of peptides and stimulation of angiogenesis after their intracellular introduction to a target cell. PR-39 derived peptides are able to interact with at least the alpha7 subunit of the proteasomes, and therefore alter the proteolytic activity of proteasomes such that a selective increased expression of specific proteins occurs. The invention includes methods for the selective inhibition of proteasome mediated peptide degradation. The method provides means for stimulating angiogenesis as required in living tissues and organs which have suffered defects or have undergone anoxia and/or infarction, myocardial infarction or chronic myocardial ischaemia of heart tissue. Examples are the myocardium, skeletal or smooth muscle, artery or vein, lung, brain, kidney, spleen, liver, gastrointestinal or nerve tissues, limbs, and extremities. A particular example is after myocardial infarction or ischaemia

Sequence 39 AA;

Query Match 100.0%; Score 155; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.2e-09;
Matches 26; Conservative 0; Mismatches 0 Indels

Qy 1 RRRRPPYLP RP RP RP PP PP FFP RL PP RI 26
|||
Db 1 RRRRPPYLP RP RP RP PP PP FFP RL PP RI 26
|||

RESULT 12
AAB84690
ID AAB84690 standard; protein: 39 AA.

AC AAB84690;

DT 17-SEP-20

Amino acid sequence of a F

PR-39; IkappaBalpha degradation; NFkappaB transcription factor;
myocardial infarction; chronic myocardial ischemia; heart disease;
anoxia.

Unidentified.

XX PN WO200147540-A1.

XX
PD 05-JUL-2001.

27-DEC-2000:

XX
PR 29-DEC-1999: 99US-00474967.

XX PA (BETH-) BETH ISRAEL DEACONESS

XX
PI
Simons M. Gao Y:XX
DR WPI: 2001-441690/XX
PT
Selective inhibition

PT IkappaBalpha and proteasomes, and altering proteolytic activity of proteasomes.

XX PS Disclosure; Page 30; 69pp; English.

The present sequence represents a PR-39 protein. The specification describes PR-39 derived peptides, which are used for selective inhibition of IkappaBalpha degradation within a targeted cell collection in-situ. The method is useful for selectively inhibiting IkappaBalpha protein degradation in situ, decreasing the activity of NFkappaB transcription factor and selective control of NFkappaB-dependent gene expression in situ. The PR-39 derived peptides are useful in the treatment of myocardial infarction, chronic myocardial ischemia of heart disease and anoxia

XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 155; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.2e-09;
Matches 26; Conservative 0; Mismatches 0; Indels

Qy

1 RRRRPPYLPRLPRPPLPFPPPLPRI 26
| | | | |
Dd

1 RRRRPPYLPRLPRPPLPFPPPLPRI 26
| | | | |

RESULT 13
ADD35364
ID ADD35364 standard; peptide; 39 AA.

XX
AC ADD35364;

DT 15-JAN-2004 (first entry)
 XX Antimicrobial peptide PR-39.
 DE intraocular pressure; glaucoma; ocular hypertension; hyperaemia;
 XX irritation; inflammation; conjunctiva; ocular cell dysplasia;
 KW iridial melanocyte hyperplasia; hyperpigmentation.
 KW Unidentified.
 XX WO2003079997-A2.
 XX 02-OCT-2003.
 XX 21-MAR-2003; 2003WO-US008935.
 XX 21-MAR-2002; 2002US-0367071P.
 XX (CAYM-) CAYMAN CHEM CO.
 XX Maxey KM, Johnson J;
 XX WPI; 2004-011506/01.
 XX Ophthalmic solution useful for the treatment of increased intraocular
 PT pressure comprises a prostaglandin of the F-series and an antimicrobial
 PT peptide.
 XX Disclosure; Page 11; 11pp; English.
 XX The invention relates to a novel ophthalmic solution comprising a
 CC prostaglandin of the F-series and an antimicrobial peptide. A solution of
 CC the invention has hypotensive and ophthalmological activity. The solution
 CC is useful for the treatment of increased intraocular pressure, such as
 CC caused by glaucoma and for the reduction of ocular hypertension. The
 CC prostaglandin and the antimicrobial peptide work synergistically, to
 CC provide beneficial reduction in the incidence of irritant and toxic side
 CC effects such as hyperaemia, irritation and inflammation of conjunctiva,
 CC ocular cell dysplasia, iridial melanocyte hyperplasia, and
 CC hyperpigmentation, associated with the prior art prostaglandin
 CC compositions. The present sequence represents an antimicrobial peptide of
 CC the invention.
 XX
 XX Sequence 39 AA;
 SQ
 Query Match 100.0%; Score 155; DB 8; Length 39;
 Best Local Similarity 100.0%; Pred. No. 7.2e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRRPRPPYLPRPPPPPPPPRLPPRI 26
 DB 1 RRRPRPPYLPRPPPPPPPPPPRLPPRI 26
 RESULT 14
 ADE86112
 ID ADE86112 standard; peptide; 39 AA.
 AC ADE86112;
 XX 29-JAN-2004 (first entry)
 DT Proline-arginine (PR)-rich antimicrobial peptide PR-39.
 DE Leukocyte superoxide anion; leukocyte O2- production;
 KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;
 KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;
 KW tissue damage; oxygen radical; antibacterial.
 XX Synthetic.
 OS US2003125249-A1.
 XX

XX 03-JUL-2003.
 PD 07-DEC-2001; 2001US-00014147.
 XX 10-APR-1995; 95US-00419066.
 PR 08-OCT-1997; 97US-00930777.
 XX (BLEC/) BLECHA.F.
 PA (SHIJ/) SHI J.
 XX Blecha F, Shi J;
 XX WPI; 2004-059188/06.
 XX Attracting leukocyte to location by administering peptide including
 PT proline-arginine-rich antimicrobial peptide or its truncated analogs to
 PT the location.
 XX Claim 2; SEQ ID NO 1; 24pp; English.
 XX The present invention relates to a method of inhibiting leukocyte
 CC superoxide anion (O2-) production and/or attracting leukocytes. The
 CC method comprises the use of proline-arginine (PR)-rich antimicrobial
 CC peptides or their truncated analogues. The method is useful for
 CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or
 CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are
 CC useful as medicaments to fight infection by attracting leukocytes to a
 CC wound site, while restricting tissue damage at the wound site caused by
 CC excessive oxygen radicals produced by these leukocytes. The present
 CC sequence represents a PR-rich antimicrobial peptide.
 XX Sequence 39 AA;
 SQ
 Query Match 100.0%; Score 155; DB 8; Length 39;
 Best Local Similarity 100.0%; Pred. No. 7.2e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRRPRPPYLPRPPPPPPPPRLPPRI 26
 DB 1 RRRPRPPYLPRPPPPPPPPRLPPRI 26
 RESULT 15
 ADL67254
 ID ADL67254 standard; peptide; 39 AA.
 XX ADL67254;
 AC 20-MAY-2004 (first entry)
 DT Antimicrobial peptide PR-39.
 DE Leucocyte ; superoxide anion; oxygen radical; proline-arginine ;
 KW antimicrobial; antioxidant ; NADPH oxidase ; p47phox; neutrophil;
 KW infection; wound ; tissue damage ; PR-39 peptide.
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..26 /label= PR-26_peptide
 FT Peptide 1..19 /label= PR-19_peptide
 FT Peptide 1..14 /label= PR-14_peptide
 FT Region 1..3 /note= "Essential for antibacterial activity"
 FT Peptide 4..26 /label= PR-23_peptide
 FT Peptide 11..26 /label= PR-16_peptide
 FT Region 20..26

FT Peptide /note= "Essential for antibacterial activity"
FT 25..39
XX /label= PR-15_peptide

PN US2004043934-A1.

XX 04-MAR-2004.

PD 28-AUG-2003; 2003US-00651147.

XX 10-APR-1995; 95US-00419066.

PR 08-OCT-1997; 97US-00930777.

XX (BLEC/) BLECHA F.

PA (SHIJ/) SHI J.

XX Blecha F, Shi J;

PI WPI; 2004-225728/21.

DR Inhibiting leukocyte oxygen radical production comprises contacting a
PT leukocyte with a peptide, where the inhibition occurs as a consequence of
PT binding between the peptide and p47phox.

XX Claim 1; SEQ ID NO 1; 24pp; English.

XX The invention relates to inhibiting leukocyte superoxide anion (O2-) production using a naturally occurring proline-arginine (PR)-rich antimicrobial peptide known as PR-39 and its truncated analogs. The method comprises contacting leukocytes with the peptide comprising 39 or 26 amino acids, for a time and under conditions effective to inhibit leukocyte superoxide anion production. The peptide inhibits the activity of NADPH oxidase responsible for anion production, by binding to Src homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or porcine leukocyte and the mammalian leukocyte is neutrophil. Another method is also disclosed which employs a PR-39 analog that comprise 16 amino acids, where the sum of the proline and arginine residues in the effective peptide is at least 66 or 74 % of the total number of amino acids. This peptide inhibits leukocyte O2- production by the effective binding to p47phox in whole cells, therefore interfering with the binding of p47phox to p22phox. At least 14 or 25% of the amino acid residues in the peptide are arginine residues. The method of the invention is useful for inhibiting leukocyte oxygen radical production. The peptides are useful as medicaments for fighting infections by attracting leukocytes to a wound site, yet restrict tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. The present sequence is PR-39 peptide.

XX SQ Sequence 39 AA;

Query Match 100.0%; Score 155; DB 8; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.2e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRRPPPPPPPPRLPPRI 26

DB 1 RRRPRPPYLPRRRPPPPPPPPRLPPRI 26

Search completed: October 26, 2005, 05:12:04
Job time : 103.345 secs

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:00:14 ; Search time 19.3818 Seconds
(without alignments)
129.071 Million cell updates/sec

Title: US-10-014-147-2
Perfect score: 155
Sequence: 1 RRRPPPYLPRPPPPFPPLPPI 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: Pirl:.*
2: Pirl2:.*
3: Pirl3:.*
4: Pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155	100.0	172	2 S68232	antimicrobial prot
2	84.5	54.5	301	2 JQ1663	hybrid proline-ric
3	82	52.9	59	2 A36589	bactenecin 7 - bov
4	80	51.6	199	2 S14981	extensin class I (
5	78	50.3	278	2 A49266	fss ligand - rat
6	77	49.7	281	2 I38707	fss ligand - human
7	75.5	48.7	1029	2 T30351	mucin-like protein
8	75	48.4	1006	2 G86292	hypothetical prote
9	74.5	48.1	212	2 S57330	cathelin-like anti
10	73.5	47.4	1460	1 EDBE1F	immediate-early pr
11	73	47.1	439	2 S51939	chitinase (EC 3.2.
12	72	46.5	415	1 A34370	acrosin (EC 3.4.21
13	71.5	46.1	42	2 B36589	bactenecin 5 - bov
14	71.5	46.1	176	2 A45328	bactenecin 5 precu
15	71.5	46.1	1958	2 B40505	hypothetical prote
16	70	45.2	389	2 S27200	proline-rich prote
17	70	45.2	2871	2 A55624	fibritin-1 precur
18	69.5	44.8	221	2 T07176	extensin homolog
19	69.5	44.8	228	2 S40463	prophenin (PF-2) p
20	69.5	44.8	491	2 T07598	proline-rich prote
21	69	44.5	254	2 T25073	hypothetical prote
22	69	44.5	296	2 A27319	gliadin - wheat
23	69	44.5	296	2 S07361	alpha/beta-gliadin
24	68.5	44.2	57	2 T10782	salivary protein p
25	68.5	44.2	79	1 FUH058	proline-rich pepti
26	68	43.9	134	2 JC5572	proline-rich prote
27	68	43.9	190	2 S68230	antimicrobial pept
28	68	43.9	239	2 T16159	hypothetical prote
29	68	43.9	588	2 T45544	hypothetical prote

hypothetical prote
spore coat protein
hypothetical prote
proline-rich prote
probable coll wall
unknown protein Fl
cysteine-rich exte
hypothetical prote
cell wall protein
probable transcrip
proline-rich prote
hypothetical prote
gene mgi protein
hypothetical prote
homoeotic protein H
spliceosome-associ

ALIGNMENTS

RESULT 1

S68232
antimicrobial protein PR-39 precursor, cathelin-associated - pig
N/Alternate names: myeloid antibacterial protein PR-39
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S68232; JN0899; I47138; S19563
R/Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 376, 130-134, 1995
A/Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni
A/Reference number: S68232; MUID:96105365; PMID:7498526
A/Accession: S68232
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-172 <ZHA>
A/Cross-references: UNIPROT:P80054; EMBL:X89201; NID:g1165150; PIDN:CAA61487.1; PID:g116:
A/Experimental source: leukocytes
R/Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
A/Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the i
A/Reference number: JN0899; MUID:94071853; PMID:8250863
A/Accession: JN0899
A/Molecule type: mRNA
A/Residues: 1-20, 'A', 22-172 <STO>
A/Cross-references: GB:I23825; NID:9435100; PIDN:AAA31109.1; PID:g435101
A/Experimental source: bone marrow cells
R/Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Boni
Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
A/Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fam
A/Reference number: I47138; MUID:95350216; PMID:7624374
A/Accession: I47138
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-28, 'T', 30-89, 'QR', 92-116, 'NDP', 120-172 <GUD>
A/Cross-references: EMBL:X67236; NID:g829142; PIDN:CAA60682.1; PID:g1051298
R/Aggerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall,
Eur. J. Biochem. 202, 849-854, 1991
A/Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of th
A/Reference number: S19563; MUID:92111534; PMID:1765098
A/Accession: S19563
A/Molecule type: protein
A/Residues: 131-169 <AGE>
A/Experimental source: intestine
C/Genetics:
A/Gene: PR39
A/Introns: 66/3; 102/3; 126/3
C/Superfamily: cathelin; cystatin homology
C/Keywords: amidated carboxyl end; antibacterial
F/1-29/Domain: signal sequence #status predicted <SIG>
F/22-129/Domain: cystatin homology <CYS>
F/30-130/Domain: propeptide #status predicted <PRO>
F/131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>

F:169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

Query Match 100.0%; Score 155; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 6e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPVPLPRPPPPPPPPRLPPRI 26
|||||
Db 131 RRRPPVPLPRPPPPPPPPRLPPRI 156
|||||

RESULT 2
JQ1663
hybrid proline-rich protein - maize
C:Species: Zea mays (maize)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JQ1663
R:Jose-Estanyol, M.; Ruiz-Avila, L.; Puigdomenech, P.
Plant Cell 4, 413-423, 1992
A:Title: A maize embryo-specific gene encodes a proline-rich and hydrophobic protein.
A:Reference number: JQ1663; MUID:92361259; PMID:1498600
A:Accession: JQ1663
A:Molecule type: DNA
A:Residues: 1-301 <JOS>
A:Cross-references: UNIPROT:Q41848; EMBL:X60432; NID:G433706; PIDN:CAA42959.1; PID:G4337
A:Experimental source: strain W64A
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 54.5%; Score 84.5; DB 2; Length 301;
Best Local Similarity 58.3%; Pred. No. 0.092;
Matches 14; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 4 PRPPVPLPRPPPPPPPPRLPP 24
|||||
Db 169 PRPPVPLPRPPPPPPPPVPP 192
|||||

RESULT 3
A36589
bactenecin 7 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-May-1997
C:Accession: A36589
R:Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
J. Biol. Chem. 265, 18871-18874, 1990
A:Title: Amino acid sequences of two proline-rich bactericins. Antimicrobial peptides of
A:Reference number: A36589; MUID:91035404; PMID:2229048
A:Accession: A36589
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-59 <FRA>
C:Superfamily: cathelin; cystatin homology

Query Match 52.9%; Score 82; DB 2; Length 59;
Best Local Similarity 68.0%; Pred. No. 0.035;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 RRRPPVPLPRPPPPPPPPRLPPRI 25
|||||
Db 2 RIRPPRLPRPPRLPPPPR 26
|||||

RESULT 4
S14981
extensin class I (clone w1-8 L) - tomato (fragment)
C:Species: Lycopersicon esculentum (tomato)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 11-Jan-2000
C:Accession: S14981
R:Shawalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
Plant Mol. Biol. 16, 547-565, 1991
A:Title: Tomato extensin and extensin-like cDNAs: structure and expression in response to
A:Reference number: S14970; MUID:91329690; PMID:1714316
A:Accession: S14981

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-199 <SHO>
A:Cross-references: EMBL:X55692
A:Experimental source: cv. UC82B
C:Superfamily: hydroxyproline-rich glycoprotein
C:Keywords: cell wall; glycoprotein; hydroxyproline

Query Match 51.6%; Score 80; DB 2; Length 199;
Best Local Similarity 60.9%; Pred. No. 0.17;
Matches 14; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 RRRPPVPLPRPPPPPPPPRLPP 24
|||||
Db 69 RRRPPPPPPPPPPPPPPPPPP 91
|||||

RESULT 5
A49266
fas ligand - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: A49266
R:Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A:Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
A:Reference number: A49266; MUID:94084792; PMID:7505205
A:Accession: A49266
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-278 <SUD>
A:Cross-references: UNIPROT:P36940; GB:U03470; NID:G440178; PIDN:AAC52129.1; PID:G440179
C:Keywords: glycoprotein; transmembrane protein

Query Match 50.3%; Score 78; DB 2; Length 278;
Best Local Similarity 62.5%; Pred. No. 0.37;
Matches 15; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 RRRPPVPLPRPPPPPPPPRLPP 24
|||||
Db 43 RRRPPPPPPPPPPPPPPPPPP 66
|||||

RESULT 6
I38707
Fas ligand - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I38707; JG2340; S57565; I38554
R:Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A:Title: Human Fas ligand: gene structure, chromosomal location and species specificity.
A:Reference number: I38707; MUID:95127560; PMID:7826947
A:Accession: I38707
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-281 <RES>
A:Cross-references: UNIPROT:P48023; EMBL:U11821; NID:G595430; PIDN:AAC50124.1; PID:G59543;
R:Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijoka, T.; Kasahara, A.; Fusamoto, H.;
Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A:Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A:Reference number: JG2340; MUID:95071350; PMID:7980502
A:Accession: JG2340
A:Molecule type: DNA
A:Residues: 1-281 <MIT>
A:Cross-references: GB:D38122; DBJ:D29820; NID:G601892; PIDN:BAA07320.1; PID:G1369902
R:Schatlein, C.E.
submitted to the EMBL Data Library, June 1995
A:Reference number: S57565
A:Accession: S57565
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-281 <SCH>

A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
R;Algeron, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
C;Genetics:
A;Gene: FasL
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;76,184,250,260/Binding site: carbohydrate (Asn) #status predicted <TM>
Query Match 49.7%; Score 77; DB 2; Length 281;
Best Local Similarity 62.5%; Pred. No. 0.47; 8; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 1; Mismatches 0; Gaps 0;
QY 1 RRRPRPPYLPRLPPPPPPPPRLPP 24
Db 42 QRRPPPPPPPPPPPPPPPPPPPPPP 65
RESULT 7
T30351
mucin-like protein - Lymantria dispar nuclear polyhedrosis virus
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30351
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr
Virology 253, 17-34, 1999
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d
A;Reference number: Z20836; MUID:99124785; PMID:9887315
A;Accession: T30351
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1029 <KUZ>
A;Cross-references: UNIPROT:Q9YMK0; EMBL:AF081810; PIDN:AAC70189.1
Query Match 48.7%; Score 75.5; DB 2; Length 1029;
Best Local Similarity 58.3%; Pred. No. 2.2; 6; Indels 1; Gaps 1;
Matches 14; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
QY 1 RRRPRPPYLPRLPPPPPPPPRLPP 24
Db 925 RKRPRYSQQPPPPPPPPPPPPPP 947
RESULT 8
G86292
hypothetical protein F7H2.17 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86292
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86292
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1006 <STO>
A;Cross-references: UNIPROT:Q9LMQ1; GB:AE005172; NID:g8927662; PIDN:AAF82153.1; GSPDB:GN

C;Genetics:
A;Map position: 1
Query Match 48.4%; Score 75; DB 2; Length 1006;
Best Local Similarity 71.4%; Pred. No. 2.5; 4; Indels 2; Gaps 1;
Matches 15; Conservative 0; Mismatches 4; Indels 2; Gaps 1;
QY 4 PRPPYLPRLPPPPPPPPRLPP 24
Db 99 PRPPPRPRPRP--SPRLPP 117
RESULT 9
S57330
cathelin-like antibacterial peptide precursor (clone C6) - pig (fragment)
N;Alternate names: antimicrobial peptide; prophenin-1
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57330; S68726
R;Strukelj, B.; Pungertar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V.
Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
A;Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte
A;Reference number: S57330; MUID:96042752; PMID:7576250
A;Accession: S57330
A;Molecule type: mRNA
A;Residues: 1-212 <STR>
A;Cross-references: UNIPROT:P51524; GB:X86031; NID:g1006756; PIDN:CAA60023.1; PID:g10067
R;Harwig, S.S.L.; Kokryakov, V.N.; Swiderek, K.M.; Aleshina, G.M.; Zhao, C.; Lehrer, R.I.
FEBS Lett. 362, 65-69, 1995
A;Title: Prophenin-1, an exceptionally proline-rich antimicrobial peptide from porcine le
A;Reference number: S68726; MUID:95212585; PMID:7698355
A;Accession: S68726
A;Molecule type: protein
A;Residues: 131-209 <HAR>
A;Experimental source: leukocytes
C;Superfamily: cathelin; cystatin homology
C;Keywords: antibacterial
F;6-113/Domain: cystatin homology <CYS>
Query Match 48.1%; Score 74.5; DB 2; Length 212;
Best Local Similarity 56.2%; Pred. No. 0.64; 4; Indels 9; Gaps 3;
Matches 18; Conservative 1; Mismatches 4; Indels 9; Gaps 3;
QY 2 RRPR-----PPYLPRLPP-PPPPPP-PRLPP 24
Db 123 RRPLRRQAFPPPPNVPGRFPFPFPFPFPFP 154
RESULT 10
EDREIF
immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser)
C;Species: suid herpesvirus 1
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: S04713
R;Cheung, A.K.
Nucleic Acids Res. 17, 4637-4646, 1989
A;Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies vi
A;Reference number: S04713; MUID:89315207; PMID:2546124
A;Accession: S04713
A;Molecule type: DNA
A;Residues: 1-1460 <CHE>
A;Cross-references: UNIPROT:P11675
C;Superfamily: herpesvirus immediate-early protein IE175
C;Keywords: DNA binding; early protein; transcription regulation
Query Match 47.4%; Score 73.5; DB 1; Length 1460;
Best Local Similarity 62.5%; Pred. No. 4.9; 7; Indels 1; Gaps 1;
Matches 15; Conservative 1; Mismatches 7; Indels 1; Gaps 1;
QY 1 RRRPRPPYLPRLPPPPPPPPRLPP 24
Db 156 RRRPRPPYLPRLPPPPPPPPPPPPPP 178

RESULT 11

S1939
 C:Species: chitinase (EC 3.2.1.14) precursor - beet
 C:Date: 28-Oct-1996 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
 C:Accession: S1939; S72315; S49025
 R:Berghlund, L.; Brunstedt, J.; Nielsen, K.K.; Chen, Z.; Mikkelsen, J.D.; Marcker, K.A.
 Plant Mol. Biol. 27, 211-216, 1995
 A>Title: A proline-rich chitinase from Beta vulgaris.
 A:Reference number: S51939; MUID:95170004; PMID:7865792
 A:Accession: S51939
 A:Molecule type: DNA
 A:Residues: 1-439 <BER>
 A:Cross-references: UNIPROT:Q42421; EMBL:X79301; NID:G488730; PID:G488731
 A>Note: the authors translated the codon TGC for residue 416 as Gly
 A:Accession: S72315
 A:Molecule type: mRNA
 A:Residues: 191-397 <BER2>
 C:Genetics:
 A:Introns: 248/1; 300/2
 C:Keywords: glycosidase; hydrolase
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-439/Product: chitinase #status predicted <MAT>
 F:183-423/Domain: plant chitinase homology <PCH>

Query Match 47.1%; Score 73; DB 2; Length 439;
 Best Local Similarity 66.7%; Pred. No. 1.8;
 Matches 14; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 PRPPYLPRLPPPPPPPPRLPP 24

DB 114 PRPPPPPPPPPPPPPPPPPPPP 134

RESULT 12

A34170
 C:Species: acrosin (EC 3.4.21.10) precursor - pig
 N:Alternate names: 53K fucose-binding protein
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
 C:Accession: A34170; S08994; S02428; S04940; S16657; S02780; S10695; S12968
 R:Baba, T.; Kaehiawabara, S.; Watanabe, K.; Itoh, H.; Michikawa, Y.; Kimura, K.; Takada, J.
 Biol. Chem. 264, 11920-11927, 1989
 A>Title: Activation and maturation mechanisms of boar acrosin zymogen based on the deduced amino acid sequence.
 A:Reference number: A34170; MUID:89308595; PMID:2745422
 A:Accession: A34170
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-415 <BAB>
 A:Cross-references: UNIPROT:P08001; GB:J04950; NID:G164702; PID:AAA31131.1; PID:G164703
 R:Cechova, D.; Toepfer-Petersen, E.; Zucker, A.; Jonakova, V.
 Biol. Chem. Hoppe-Seyler 371, 317-323, 1990
 A>Title: Is sperminogen a modified proacrosin? Isolation, purification, and partial characterization.
 A:Reference number: S08994; MUID:90253655; PMID:2111146
 A:Accession: S08994
 A:Molecule type: protein
 A:Residues: 'X', 18, 'X', 20-25, 'X', 27-32, 'X', 34-38, 'X', 40-50 <CEC>
 R:Toepfer-Petersen, E.; Henschen, A.
 FEBS Lett. 226, 38-42, 1987
 A>Title: Acrosin shows zona and fucose binding, novel properties for a serine proteinase
 A:Reference number: S02428; MUID:88083633; PMID:3480243
 A:Accession: S02428
 A:Molecule type: protein
 A:Residues: 17-32/40-55 <TOE>
 R:Adham, I.M.; Klemm, U.; Maier, W.M.; Hoyer-Fender, S.; Tsousidou, S.; Engel, W.
 Eur. J. Biochem. 182, 563-568, 1989
 A>Title: Molecular cloning of preproacrosin and analysis of its expression pattern in spermatogenesis.
 A:Reference number: S04940; MUID:89325301; PMID:2502391
 A:Accession: S04940
 A:Molecule type: mRNA
 A:Residues: 1-7, 9-210, 'Q', 212-216, 'VT', 219-346, 'A', 348-388, 390-393, 'GN', 396, 'LVE', 399-400
 A:Cross-references: EMBL:X14844

A>Note: the authors translated the codon CCT for residue 240 as Ala, GCC for residue 264
 R:Adham, I.M.
 Submitted to the EMBL Data Library, March 1989
 A:Reference number: S16657
 A:Accession: S16657
 A:Molecule type: mRNA
 A:Residues: 1-7, 9-210, 'Q', 212-216, 'VT', 219-346, 'A', 348-388, 390-398, 'KELL', <AD2>
 A:Cross-references: EMBL:X14844; NID:G1867; PID:CAA32948.1; PID:G1868
 A>Note: the difference at the carboxyl end is due to a frameshift error
 R:Baba, T.; Michikawa, Y.; Kawakura, K.; Arai, Y.
 FEBS Lett. 244, 132-136, 1989

A>Title: Activation of boar proacrosin is effected by processing at both N- and C-termini
 A:Reference number: S02780; MUID:89171246; PMID:2494060
 A:Accession: S02780
 A:Molecule type: protein
 A:Residues: 17-69 <BA2>
 R:Toepfer-Petersen, E.; Steinberger, M.; von Eschenbach, C.E.; Zucker, A.
 FEBS Lett. 265, 51-54, 1990
 A>Title: Zona pellucida-binding of boar sperm acrosin is associated with the N-terminal
 A:Reference number: S10695; MUID:90306316; PMID:2365054
 A:Accession: S10695
 A:Molecule type: protein
 A:Residues: 40-62 <TO2>

R:Toepfer-Petersen, E.; Calvete, J.; Schaefer, W.; Henschen, A.
 FEBS Lett. 275, 139-142, 1990
 A>Title: Complete localization of the disulfide bridges and glycosylation sites in boar
 A:Reference number: S12968; MUID:91085546; PMID:2261983
 A:Accession: S12968
 A:Molecule type: protein
 A:Residues: 17-29;34-66;68-91;94-121;123-166;171-184;190-207;209-216;219-228;231-245;248-

C:Superfamily: acrosin; trypsin homology
 C:Keywords: glycoprotein; hydrolase; serine proteinase; sperm
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-415/Product: acrosin #status experimental <MAT>
 F:17-39/Product: acrosin light (A) chain #status experimental <LCH>
 F:40-415/Product: acrosin heavy (B) chain #status experimental <HCH>
 F:40-283/Domain: trypsin homology <TRY>
 F:300-374/Region: proline-rich
 F:19,208/Binding site: carbonylhydrate (Asn) (covalent) #status experimental
 F:22-152,26-160,71-87,175-244,207-223,234-264/Disulfide bonds: #status experimental
 F:86,140,238/Active site: His, Asp, Ser #status predicted

Query Match 46.5%; Score 72; DB 1; Length 415;
 Best Local Similarity 63.6%; Pred. No. 2.1;
 Matches 14; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RRPYPPLPRPPPPPPPPRLPP 24

DB 338 RRPYPAPPPPPPPPPPPPPPP 359

RESULT 13

bactenecin 5 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 08-Dec-1995
 C:Accession: B36589
 R:Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
 J. Biol. Chem. 265, 18871-18874, 1990
 A>Title: Amino acid sequences of two proline-rich bactericins. Antimicrobial peptides of
 A:Reference number: A36589; MUID:91035404; PMID:2229048
 A:Accession: B36589
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-42 <FRA>
 C:Superfamily: cathelin; cystatin homology

Query Match 46.1%; Score 71.5; DB 2; Length 42;
 Best Local Similarity 57.1%; Pred. No. 0.26;
 Matches 16; Conservative 1; Mismatches 6; Indels 5; Gaps 2;

QY 2 RRPYPPLPRPPPPPPPPRLPP 24

DB 338 RRPYPAPPPPPPPPPPPPPPP 359

Db 7 RRPPIRPPFPFPPPIRPPPIRPP 34

RESULT 14

A45328
bactenecin 5 precursor - bovine
N:Alternate names: Bac5; neutrophil antibiotic protein 5
C:Species: Bos primigenius taurus (cattle)
C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: A45328
R:Zanetti, M.; Del Sal, G.; Storici, P.; Schneider, C.; Roméo, D.
J. Biol. Chem. 268, 522-526, 1993
A:Title: The cDNA of the neutrophil antibiotic Bac5 predicts a pro-sequence homologous to
A:Reference number: A45328; MUID:93107055; PMID:8416958
A:Accession: A45328
A:Molecule type: mRNA
A:Residues: 1-176 <ZAN>
A:Cross-references: UNIPROT:P19660; GB:I02650; NID:G162730; PIDN:AAA30404.1; PID:G162731
A:Note: sequence extracted from NCBI backbone (NCBIP:121443)
C:Superfamily: cathelin; cystatin homology
C:Keywords: amidated carboxyl end; antibacterial
F:1-29/Domain: signal sequence #status predicted <SIG>
F:22-129/Domain: cystatin homology <CYS>
F:30-130/Domain: propeptide #status predicted <PRO>
F:131-173/Product: neutrophil antibiotic protein Bac5 #status predicted <MAT>
F:173/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

Query Match 46.1%; Score 71.5; DB 2; Length 176;
Best Local Similarity 57.1%; Pred. No. 1.1;
Matches 16; Conservative 1; Mismatches 6; Indels 5; Gaps 2;

QY 2 RRP--RPPYLPRPP---PPFPFPRLPP 24

Db 137 RRPPIRPPFPFPPPIRPPPIRPP 164

RESULT 15

B40505
hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhuser or Becker)
C:Species: suid herpesvirus 1
C>Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 09-Jul-2004
C:Accession: B40505
R:Cheung, A.K.
J. Virol. 65, 5260-5271, 1991
A:Title: Cloning of the latency gene and the early protein 0 gene of pseudorabies virus.
A:Reference number: A40505; MUID:91374576; PMID:1654441
A:Accession: B40505
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1958 <CHE>
A:Cross-references: UNIPROT:Q69340; GB:M57505; NID:G334066; PIDN:AAA47468.1; PID:G334068
C:Superfamily: pseudorabies virus 1 nuclear antigen

Query Match 46.1%; Score 71.5; DB 2; Length 1958;
Best Local Similarity 62.5%; Pred. No. 10;
Matches 15; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 RRRPRPPYLRPPPPFPFPPRLPP 24

Db 477 RDRPRPP-SPPRRPPPLPPPPPP 499

Search completed: October 26, 2005, 05:19:58
Job time : 20.3818 secs

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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:52:03 ; Search time 90.0546 Seconds
(without alignments)
147.844 Million cell updates/sec

Title: US-10-014-147-2

Perfect score: 155

Sequence: 1 RRRPRPPYLPRPPPPPPPPRPPRI 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	100.0	172	PR39_PIG	P80054 sus scrofa
2	85.5	55.2	228	Q6Z8Z0	P62840 oryza sativ
3	84.5	54.5	301	Q41848	Q41848 zea mays (m
4	82	52.9	190	1 BCT7 BOVIN	P19661 bos taurus
5	81	52.3	514	Q6QTF1	Q6qtf1 arabidopsis
6	81	52.3	520	Q9LV14	Q9lv14 arabidopsis
7	79	51.0	333	Q9X1Z3	Q9xi23 oryza sativ
8	78	50.3	278	1 TNF6 RAT	P36940 rattus norv
9	77.5	50.0	625	2 Q8S9B5	Q8s9b5 volvox cart
10	77	49.7	281	1 TNF6 HUMAN	P48023 homo sapien
11	77	49.7	1395	2 Q7SC01	Q7sc01 neurospora
12	76.5	49.4	185	2 Q94JF6	Q94jfe oryza sativ
13	76	49.0	183	2 Q94J98	Q94j98 oryza sativ
14	76	49.0	409	2 Q9SBN1	Q9sbm1 volvox cart
15	75.5	48.7	1029	2 Q9YXX0	Q9ymx0 lymantria d
16	75	48.4	1006	2 Q9LMQ1	Q9lmql arabidopsis
17	74.5	48.1	212	1 PF11 PIG	P51524 sus scrofa
18	74.5	48.1	342	2 Q6ZD62	Q6zdd2 oryza sativ
19	74.5	48.1	816	2 Q7Q3J9	Q7q3j9 anopheles g
20	74	47.7	1134	2 Q96JH1	Q96jh1 homo sapien
21	73	47.1	439	2 Q42421	Q42421 beta vulgar
22	73	47.1	548	2 Q6ESK7	Q6esk7 oryza sativ
23	72.5	46.8	236	2 Q657Y0	Q657y0 oryza sativ
24	72.5	46.8	480	2 Q740X0	Q740x0 mycobacteri
25	72	46.5	147	2 Q6F392	Q6f392 oryza sativ
26	72	46.5	415	1 ACRO_PIG	P08001 sus scrofa
27	72	46.5	1200	2 Q96PN7	Q9epn7 homo sapien
28	72	46.5	2374	2 Q7SBD3	Q7abd3 neurospora
29	71.5	46.1	176	1 BCT5 BOVIN	P19660 bos taurus
30	71.5	46.1	591	2 P79817	P79817 oryzias lat
31	71.5	46.1	666	2 Q8JHT8	Q8jht8 oryzias lat

32 71.5 46.1 670 2 Q8J122 Q8j122 oryzias lat
33 71.5 46.1 1958 2 Q69340 Q69340 suid herpes
34 71 45.8 103 2 Q99FW9 Q99fw9 human papil
35 71 45.8 687 2 Q948Y7 Q948y7 volvox cart
36 70.5 45.5 146 2 Q7Q8P5 Q7q8p5 anopheles g
37 70.5 45.5 206 2 Q74C95 Q74c95 geobacteri s
38 70.5 45.5 210 2 Q6ZJE9 Q6zje9 oryza sativ
39 70.5 45.5 280 1 TNF6 CERTO Q9bdn1 cercocobus
40 70.5 45.5 782 1 SX30_MOUSE Q8sgw4 mus musculus
41 70.5 45.5 3409 2 Q6SSE6 Q6sae6 chlamydomon
42 70 45.2 273 2 Q82PZ6 Q82pz6 streptomyce
43 70 45.2 366 2 Q84X72 Q84x72 chlamydomon
44 70 45.2 401 2 Q8S054 Q8s054 oryza sativ
45 70 45.2 605 2 Q9Q5L3 Q9q5l3 cercopithec

ALIGNMENTS

RESULT 1

PR39_PIG
ID PR39_PIG STANDARD; PRT; 172 AA.
AC P80054; Q9TR84;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antibacterial protein PR-39 precursor.
GN Name=PR39;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95350216; PubMed=7624374;
RA Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,
RA Andersson L., Boman H.G.;
RT "Structure of the gene for porcine peptide antibiotic PR-39, a
RT cathelin gene family member: comparative mapping of the locus for the
RT human peptide antibiotic FALL-39";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=94071853; PubMed=8250863;
RA Storici P., Zanetti M.;
RT "A cDNA derived from pig bone marrow cells predicts a sequence
RT identical to the intestinal antibacterial peptide PR-39";
RL Biochem. Biophys. Res. Commun. 196:1058-1065(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;
RA Zhao C., Ganz T., Lehrer R.I.;
RT "Structures of genes for two cathelin-associated antimicrobial
RT peptides: prophenin-2 and PR-39";
RL FEBS Lett. 376:130-134(1995).
RN [4]
RP SEQUENCE OF 131-169.
RC TISSUE=Intestine;
RX MEDLINE=92111534; PubMed=1765098;
RA Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
RA Mutt V., Joernvall H.;
RT "Amino acid sequence of PR-39. Isolation from pig intestine of a new
RT member of the family of proline-arginine-rich antibacterial
RT peptides";
RL Eur. J. Biochem. 202:849-854(1991).
RN [5]
RP SEQUENCE OF 131-164, AND FUNCTION.
RC TISSUE=Neutrophils;
RX MEDLINE=95088504; PubMed=7996056;
RA Shi J., Ross C.R., Chengappa M.M., Blecha F.;
RT "Identification of a proline-arginine-rich antibacterial peptide from

RT neuropeptides that is analogous to PR-39, an antibacterial peptide from
 the small intestine.";
 RL J. Leukoc. Biol. 56:807-811(1994).
 CC -!- FUNCTION: Exerts a potent antimicrobial activity against both
 CC E.coli and B.megaterium.
 CC -!- TISSUE SPECIFICITY: Small intestine and bone marrow.
 CC -!- SIMILARITY: Belongs to the cathelicidin family.
 CC -----
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 DR EMBL; X87236; CAA60682.1; -;
 DR EMBL; I23825; AAA31109.1; -;
 DR EMBL; X89201; CAA61487.1; -;
 DR PIR; S68232; S68232.
 DR HSSP; P32196; 1KWI.
 DR InterPro; IPR001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidin; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 DR Amidation; Antibiotic; Direct protein sequencing;
 KW Pyrrolidone carboxylic acid; Signal.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 130 Antibacterial protein PR-39.
 FT CHAIN 131 169 Pyrrolidone carboxylic acid (By
 FT MOD_RES 30 30 similarity).
 FT DISULFID 85 96 By similarity.
 FT DIPEPTIDE 107 124 By similarity.
 FT MOD_RES 169 169 Proline amide (G-170 provides amide
 FT group).
 FT CONFLICT 21 21 G -> A (in Ref. 2).
 FT CONFLICT 29 29 A -> T (in Ref. 1).
 FT CONFLICT 90 91 RQ -> QR (in Ref. 1).
 FT CONFLICT 117 119 IHS -> NDP (in Ref. 1).
 FT CONFLICT 157 157 P -> I (in Ref. 5).
 SQ SEQUENCE 172 AA; 19476 MW; 994B792798C0E133 CRC64;
 Query Match 100.0%; Score 155; DB 1; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRRPRPPLPRPRPPPPPPPPRLPPRI 26
 DB 131 RRRPRPPLPRPRPPPPPPPPRLPPRI 156
 RESULT 2
 Q62820 PRELIMINARY; PRT; 228 AA.
 AC Q62820;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein P0501G04.17.
 GN Name=P0501G04.17;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF004752; BAD07841.1; -;
 KW Hypothetical protein.

SQ SEQUENCE 228 AA; 24277 MW; EACA08812E410106 CRC64;
 Query Match 55.2%; Score 85.5; DB 2; Length 228;
 Best Local Similarity 55.2%; Pred. No. 0.58;
 Matches 16; Conservative 3; Mismatches 5; Indels 5; Gaps 1;
 QY 2 RRRPRPY-----LPRPRPPPPPPPPRLPPR 25
 DB 21 RRRPRPWSASHRLPKPPPTWSPRP 49
 RESULT 3
 Q41848 PRELIMINARY; PRT; 301 AA.
 AC Q41848;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Prolin rich protein.
 GN Name=PRP;
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OC NCB1_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W64A;
 RA Jose-Estanyol M., Ruiz-Avila L., Puigdomenech P.;
 RT "A maize embryo-specific gene encodes a proline-rich and hydrophobic
 RT protein.";
 RL Plant Cell 4:413-423(1992).
 DR EMBL; X60432; CAA42959.1; -;
 DR PIR; JQ1663; JQ1663.
 DR HSSP; P24337; LHYP.
 DR InterPro; IPR003612; AAI.
 DR Pfam; PF00234; tryp_alpha_amy1; 1.
 DR SMART; SMO0499; AAI; 1.
 SQ SEQUENCE 301 AA; 31647 MW; 884EB70854D28C2E CRC64;
 Query Match 54.5%; Score 84.5; DB 2; Length 301;
 Best Local Similarity 58.3%; Pred. No. 0.95;
 Matches 14; Conservative 3; Mismatches 4; Indels 3; Gaps 1;
 QY 4 PRPPYL---PRPRPPPPPPPPRLPP 24
 DB 169 PTPVVPPTPRSPPPPPVVPVVP 192
 RESULT 4
 BCT7 BOVIN STANDARD; PRT; 190 AA.
 ID BCT7 BOVIN
 AC P19661;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Bactenecin 7 precursor (BAC7) (PR-59).
 GN Name=BAC7;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCB1_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=95010707; PubMed=7925973; DOI=10.1016/0014-5793(94)00954-6;
 RA Scocchi M., Romeo D., Zanetti M.;
 RT "Molecular cloning of Bact7, a proline- and arginine-rich antimicrobial
 RL peptide from bovine neutrophils.";
 RL FEBS Lett. 352:197-200(1994).
 RN [2]

GN Name=ELF5;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RN [1]
 RN
 RN
 RP SEQUENCE FROM N.A.
 RX PubMed=15125772; DOI=10.1111/j.1365-3113X.2004.02072.x;
 RA Noh Y.-S., Bizzell C.M., Noh B., Schomburg F.M., Amasino R.M.;
 RL "EARLY FLOWERING 5 acts as a floral repressor in Arabidopsis.";
 RT Plant J. 38:664-672(2004).
 DR EMBL; AY526094; RAS19471.1; -;
 SQ SEQUENCE 514 AA; 55467 MW; 04F230C24563BF2D CRC64;

 Query Match 52.3%; Score 81; DB 2; Length 514;
 Best Local Similarity 66.7%; Pred. No. 3.4;
 Matches 14; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

 QY 4 PRPPYLRPRPPPPPPPPRLPP 24
 DB 372 PRPPYGPPEGPPPMRPPPLPP 392
 ||||| ||||| |||||

 RESULT 6
 Q9LV14 PRELIMINARY; PRT; 520 AA.
 ID Q9LV14;
 AC Q9LV14;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MRG21
 DE (AT5G2640/MRG21.6).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 OC
 ON NCBI_TaxID=3702;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RL "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty Pl and TAC
 RT clones.";
 RN DNA Res. 7:31-63(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,
 RA Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
 RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
 RA Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M.,
 RA Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W.,
 RA Theologis A., Ecker J.R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Huan V.W., Lam B.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB020751; BAA97211.1; -;
 DR EMBL; AF361818; AAK32831.1; -;
 DR EMBL; BT002708; AAO11624.1; -;
 SQ SEQUENCE 520 AA; 55996 MW; BB6652EE0BE93E2D CRC64;

 Query Match 52.3%; Score 81; DB 2; Length 520;

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Best Local Similarity 66.7%; Pred. No. 3.5; Mismatches 7; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 4 PRPPYLPRLPRPPPPPPPPRLPP 24
DB 378 PRPPYGPPLPPPPPPPPPPRLPP 398

RESULT 7
Q9X123
ID Q9X123 PRELIMINARY; PRT; 333 AA.
AC Q9X123;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to Zea mays PRP gene.(X60432).
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Nagamura Y., Yamamoto K.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB023482; BAA78762.1; -.
DR HSSP; P24337; 1HYP.
DR Gramene; Q9X123; -.
DR InterPro; IPR003612; AAI.
DR Pfam; PF00234; Tryp_alpha_aml1; 1.
DR SMART; SM00499; AAI; 1.
DR SMART; SM00207; TNF; 1.
SQ SEQUENCE 333 AA; 34823 MW; 268DEC74E20E8194 CRC64;

Query Match 51.0%; Score 79; DB 2; Length 333;
Best Local Similarity 50.0%; Pred. No. 3.5;
Matches 14; Conservative 3; Mismatches 9; Indels 2; Gaps 1;

QY 1 RRRPPYLPRLPRPP--PPFPRLPPRI 26
DB 172 RPPPTPPYVPSPPYVPPYVPPPTPPYV 199

RESULT 8
TNF6_RAT
ID TNF6_RAT STANDARD; PRT; 278 AA.
AC P36940;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand).
GN Name=TNFsf6; Synonyms=Apt1lg1, Fas1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94084792; PubMed=7505205; DOI=10.1016/0092-8674(93)90326-L;
RA Suda T., Takahashi T., Golstein P., Nagata S.;
RT "Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor family.";
RL Cell 75:1169-1178(1993).
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance. In the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/Dcr3 modulates its effects (By similarity).
CC -!- SUBUNIT: Homotrimer (Probable).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).

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-!- TISSUE SPECIFICITY: Expressed in activated splenocytes and thymocytes. Moderate or weak expression found in small intestines, kidney and lung.
-!- INDUCTION: By PMA/ionomycin and concavalin/interleukin-2.
-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
-!- SIMILARITY: Belongs to the tumor necrosis factor family.

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EMBL; U03470; AAC52129.1; -.
PIR; A49266; A49266.
HSSP; P50591; 1DG6.
RGD; 3880; Thfsf6.
DR InterPro; IPR008064; Fas_ligand.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00499; TNF_2; 1.
KW Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
CHAIN 1 278
FT CHAIN 127 278
FT CHAIN 127 278
FT DOMAIN 1 77
FT TRANSMEM 78 99
FT SIGNAL-ANCHOR 1 77
FT SIGNAL-ANCHOR 78 99
FT DOMAIN 100 278
FT DOMAIN 4 69
FT DOMAIN 45 58
FT SITE 126 127
FT SITE 126 127
FT DISULFID 199 230
FT CARBOHYD 116 116
FT CARBOHYD 247 247
FT CARBOHYD 257 257
FT CARBOHYD 257 257
SQ SEQUENCE 278 AA; 31140 MW; 2898E18A862CEAC6 CRC64;

Query Match 50.3%; Score 78; DB 1; Length 278;
Best Local Similarity 52.5%; Pred. No. 3.6;
Matches 15; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 RRRPPYLPRLPRPPPPPPPPRLPP 24
DB 43 RPPPPPPPPSPLPPPSQPPPLPP 66

RESULT 9
Q8S9B5
ID Q8S9B5 PRELIMINARY; PRT; 625 AA.
AC Q8S9B5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Matrix metalloproteinase.
GN Name=1892;
OS Volvox carteri f. nagariensis.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Volvocaceae; Volvox.
OX NCBI_TaxID=3068;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=HK10;
RX MEDLINE=21888633; PubMed=11891059; DOI=10.1016/S0378-1119(01)00899-X;
RA Shimizu T., Inoue T., Shirashi H.;
RT "Cloning and characterization of novel extensin-like cDNAs that are
RT expressed during late somatic cell phase in the green alga Volvox
RT carteri.";
RL Gene 284:179-187(2002).
DR EMBL: AB070344; BAB85218.1; -
DR InterPro: IPR008752; Peptidase M11.
DR InterPro: IPR006025; Pept M Zn BS.
DR Pfam: PF05548; Peptidase M11.
DR PROSITE: PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 625 AA; 67803 MW; 050420F8A8A013BD CRC64;

Query Match 50.0%; Score 77.5; DB 2; Length 625;
Best Local Similarity 68.0%; Pred. No. 8;
Matches 17; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

.QY 2 RRRPPVLP-PPPPPPPPRLPPR 25
Db 586 RPTPPQKPPRPPPP--PPRPPR 608

RESULT 10
TNF6 HUMAN STANDARD; PRT; 281 AA.
ID TNF6 HUMAN Q9BZF9;
AC P48023; Q9BZF9;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (Apoptosis antigen ligand) (APTL) (CD178 antigen).
GN Names=TNFRSF6; Synonyms=APTLG1, FASL;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
RT lymphocytes.";
RL J. Exp. Med. 181:71-77(1995).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95071350; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: gene structure, chromosomal location and species
RT specificity.";
RL Int. Immunol. 6:1567-1574(1994).
[3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Schaeublein C.E., Poehmann E., Philippson P., Eibel H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioaka T., Kasahara A.,
RA Fuusamoto H., Kanada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT infection.";
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
[5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;
RT "Isolation and characterization of a new naturally occurring variant of
RT human Fas ligand that is expressed only in membrane bound form.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.

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RA Wilkinson J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Blood;
RL MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[8]
RP SEQUENCE OF 1-10 FROM N.A.
RL TISSUE=Blood;
RA Matsumura M., Nakanishi Y., Ohba Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
[9]
RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
RX MEDLINE=97373583; PubMed=9228058; DOI=10.1074/jbc.272.30.18827;
RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
RA Tersikh A., Peitsch M.C., Tschopp J.;
RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
RL J. Biol. Chem. 272:18827-18833(1997).
[10]
RP PROCESSING.
RX MEDLINE=98087475; PubMed=9427603;
RA Tanaka M., Itai T., Adachi M., Nagata S.;
RT "Downregulation of Fas ligand by shedding.";
RL Nat. Med. 4:31-36(1998).
CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
CC modulates its effects.
CC -1- SUBUNIT: Homotrimer (Probable).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. May be released
CC into the extracellular fluid, probably by cleavage from the cell
CC surface.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P48023-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P48023-2; Sequence=VSP_006443, VSP_006444;
CC -1- PTM: N-glycosylated.
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing.
CC -1- DISEASE: Defects in TNFRSF6 are a cause of autoimmune
CC lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome
CC involving hemolytic anemia and thrombocytopenia with massive
CC lymphadenopathy and splenomegaly.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -1- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674.g.htm".
CC -----

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RP SEQUENCE FROM N.A.
RX MEDLINE=99124785; PubMed=9887315; DOI=10.1006/viro.1998.9469;
RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:02:04 ; Search time 26.7091 Seconds
(without alignments)
72.667 Million cell updates/sec

Title: US-10-014-147-2

Perfect score: 155
Sequence: 1 RRRPPYLPRLPPPPPPPPRLPPRI 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
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3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155	100.0	26	2	US-08-419-066-2
2	155	100.0	26	3	US-09-024-975-2
3	155	100.0	26	4	US-08-930-777A-2
4	155	100.0	38	4	US-09-739-535-1
5	155	100.0	39	1	US-08-162-052-1
6	155	100.0	39	1	US-08-310-722-1
7	155	100.0	39	2	US-08-419-066-1
8	155	100.0	39	2	US-08-728-333-1
9	155	100.0	39	3	US-09-024-975-1
10	155	100.0	39	4	US-08-930-777A-1
11	155	100.0	39	5	PCT-US95-12080-1
12	140	90.3	23	4	US-08-930-777A-3
13	116	74.8	19	4	US-08-930-777A-4
14	96	61.9	16	3	US-09-024-975-3
15	96	61.9	16	4	US-08-930-777A-5
16	83	53.5	14	3	US-09-024-975-4
17	83	53.5	14	4	US-08-930-777A-7
18	82	52.9	59	4	US-09-030-619-163
19	78	50.3	278	3	US-08-339-214-16
20	78	50.3	278	3	US-08-339-214-26
21	78	50.3	278	4	US-09-131-237C-6
22	78	50.3	278	4	US-09-246-129B-6
23	77	49.7	129	4	US-08-968-686-2
24	77	49.7	265	4	US-08-968-686-10
25	77	49.7	268	4	US-08-968-686-6
26	77	49.7	281	2	US-08-810-453-2
27	77	49.7	281	3	US-08-815-190A-2

28	77	49.7	281	3	US-09-290-640-25	Sequence 25, Appl
29	77	49.7	281	3	US-09-479-524-3	Sequence 3, Appl
30	77	49.7	281	3	US-08-339-214-8	Sequence 8, Appl
31	77	49.7	281	3	US-08-339-214-30	Sequence 30, Appl
32	77	49.7	281	4	US-09-589-287B-6	Sequence 6, Appl
33	77	49.7	281	4	US-09-157-864-10	Sequence 10, Appl
34	77	49.7	281	4	US-09-006-755B-1	Sequence 1, Appl
35	77	49.7	281	4	US-09-027-287-6	Sequence 6, Appl
36	77	49.7	281	4	US-09-252-656B-6	Sequence 6, Appl
37	77	49.7	281	4	US-08-968-685-12	Sequence 12, Appl
38	77	49.7	281	4	US-08-968-685-12	Sequence 6, Appl
39	77	49.7	281	4	US-09-589-286A-6	Sequence 6, Appl
40	77	49.7	281	4	US-09-523-323-6	Sequence 25, Appl
41	77	49.7	281	4	US-09-665-615B-25	Sequence 6, Appl
42	77	49.7	281	4	US-09-005-874-6	Sequence 6, Appl
43	77	49.7	281	4	US-09-255-794A-6	Sequence 6, Appl
44	77	49.7	281	4	US-09-507-968D-6	Sequence 6, Appl
45	77	49.7	281	5	PCT-US95-00362-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-419-066-2
; Sequence 2, Application US/08419066
; Patent No. 5810993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-2

Query Match 100.0%; Score 155; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. NO. 9e-10;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRPPYLPRLPPPPPPPPRLPPRI 26

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Db      1 RRRPPVLPRLPPPPPPPPPPRLPPRI 26
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RESULT 2
US-09-024-975-2
; Sequence 2, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-024-975-2
Query Match      100.0%; Score 155; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 9e-10;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRPPVLPRLPPPPPPPPPPRLPPRI 26
|||||
Db      1 RRRPPVLPRLPPPPPPPPPPRLPPRI 26
|||||
RESULT 3
US-08-930-777A-2
; Sequence 2, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-930-777A-2
Query Match      100.0%; Score 155; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 9e-10;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRPPVLPRLPPPPPPPPPPRLPPRI 26
|||||
Db      1 RRRPPVLPRLPPPPPPPPPPRLPPRI 26
|||||
RESULT 4
US-09-739-535-1
; Sequence 1, Application US/09739535
; Patent No. 6794490
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/739,535
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-739-535-1
Query Match      100.0%; Score 155; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRPPVLPRLPPPPPPPPPPRLPPRI 26
|||||
Db      1 RRRPPVLPRLPPPPPPPPPPRLPPRI 26
|||||
RESULT 5
US-08-162-052-1
; Sequence 1, Application US/08162052
; Patent No. 5489575
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong-Youn
; APPLICANT: BOMAN, Hans G
```

APPLICANT: MUTT, Viktor
APPLICANT: JORNVAL, Hans
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,052
FILING DATE: 02-JUN-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9101838-2
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92-22578
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 003300-299
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-162-052-1
Query Match 100.0%; Score 155; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPPYLPRLPPPPPPRLPPRI 26
DB 1 RRRPPYLPRLPPPPPPRLPPRI 26
RESULT 6
US-08-310-722-1
Sequence 1, Application US/08310722
Patent No. 5654273
GENERAL INFORMATION:
APPLICANT: Gallo, Richard L.
APPLICANT: Klagsbrun, Michael
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/310,722
FILING DATE: 22-SEP-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: CMCC379
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Lee, Jong-Youn
AUTHORS: Boman, Hans G.
AUTHORS: Mutt, Viktor
AUTHORS: Jornvall, Hans
TITLE: No. 5654273el Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-310-722-1
Query Match 100.0%; Score 155; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPPYLPRLPPPPPPRLPPRI 26
DB 1 RRRPPYLPRLPPPPPPRLPPRI 26
RESULT 7
US-08-419-066-1
Sequence 1, Application US/08419066
Patent No. 5830993
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
ADDRESSEE: Collins
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,066
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 23625
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-930-777A-1

Query Match 100.0%; Score 155; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPYLPRLPPPPPPPPRLPPRI 26
Db 1 RRRPPYLPRLPPPPPPPPRLPPRI 26

RESULT 11
PCT-US95-12080-1
Sequence 1, Application PC/TUS9512080
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabat
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12080
FILING DATE:
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-815-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Lee, Jong-Youn
AUTHORS: Boman, Hans G.
AUTHORS: Mutt, Viktor
AUTHORS: Jornvall, Hans
TITLE: Novel Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
PCT-US95-12080-1

Query Match 100.0%; Score 155; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPYLPRLPPPPPPPPRLPPRI 26
Db 1 RRRPPYLPRLPPPPPPPPRLPPRI 26

RESULT 12
US-08-930-777A-3
Sequence 3, Application US/08930777A
Patent No. 6713605
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-930-777A-3

Query Match 90.3%; Score 140; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PRPPYLPRLPPPPPPPPRLPPRI 26

<p>Db</p> <p>1 PRPPYLPRLPRPPFPPLPPI 23</p> <p>RESULT 13</p> <p>US-08-930-777A-4</p> <p>; Sequence 4, Application US/08930777A</p> <p>; Patent No. 6713605</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Blecha, Frank</p> <p>; APPLICANT: Shi, Jishu</p> <p>; TITLE OF INVENTION: Synthetic Antimicrobial Peptide</p> <p>; NUMBER OF SEQUENCES: 9</p> <p>; CORRESPONDENCE ADDRESS:</p> <p>; ADDRESSEE: Hovey, Williams, Timmons & Collins</p> <p>; STREET: 2405 Grand Blvd., Ste. 400</p> <p>; CITY: Kansas City</p> <p>; STATE: Missouri</p> <p>; COUNTRY: U.S.A.</p> <p>; ZIP: 64108</p> <p>; COMPUTER READABLE FORM:</p> <p>; MEDIUM TYPE: Floppy disk</p> <p>; OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>; SOFTWARE: PatentIn Release #1.0, Version #1.25</p> <p>; CURRENT APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US/08/930,777A</p> <p>; FILING DATE: October 8, 1997</p> <p>; CLASSIFICATION: 530</p> <p>; PRIOR APPLICATION DATA:</p> <p>; APPLICATION NUMBER: PCT/US96/04674</p> <p>; FILING DATE: April 10, 1996</p> <p>; NAME: COLLINS, JOHN M.</p> <p>; REGISTRATION NUMBER: 26,262</p> <p>; REFERENCE/DOCKET NUMBER: 23625-A</p> <p>; TELECOMMUNICATION INFORMATION:</p> <p>; TELEPHONE: (816) 474-9050</p> <p>; TELEFAX: (816) 474-9057</p> <p>; INFORMATION FOR SEQ ID NO: 4:</p> <p>; LENGTH: 19 amino acids</p> <p>; TYPE: amino acid</p> <p>; TOPOLOGY: linear</p> <p>; MOLECULE TYPE: peptide</p> <p>US-08-930-777A-4</p>	<p>Query Match 74.8%; Score 116; DB 4; Length 19;</p> <p>Best Local Similarity 100.0%; Pred. No. 5.9e-06;</p> <p>Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 1 RRRPPYLPRLPRPPFPFP 19</p> <p> </p> <p>Db 1 RRRPPYLPRLPRPPFPFP 19</p> <p>RESULT 14</p> <p>US-09-024-975-3</p> <p>; Sequence 3, Application US/09024975</p> <p>; Patent No. 613323</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: ROSS, CHRISTOPHER R.</p> <p>; APPLICANT: BLECHA, FRANK</p> <p>; APPLICANT: SHI, JISHU</p> <p>; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY</p> <p>; NUMBER OF SEQUENCES: 11</p> <p>; CORRESPONDENCE ADDRESS:</p> <p>; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS</p> <p>; STREET: 2405 GRAND BLVD., SUITE 400</p> <p>; CITY: KANSAS CITY</p> <p>; STATE: MO</p> <p>; COUNTRY: USA</p>
<p>ZIP: 64108</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: PatentIn Release #1.0, Version #1.30</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/09/024,975</p> <p>FILING DATE:</p> <p>CLASSIFICATION:</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US 08/802,306</p> <p>FILING DATE: 18-FEB-1997</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: COLLINS, JOHN M.</p> <p>REGISTRATION NUMBER: 26,262</p> <p>REFERENCE/DOCKET NUMBER: 25585-A</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 816/474-9050</p> <p>TELEFAX: 816/474-9057</p> <p>INFORMATION FOR SEQ ID NO: 3:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 16 amino acids</p> <p>TYPE: amino acid</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: peptide</p> <p>US-09-024-975-3</p>	<p>Query Match 61.9%; Score 96; DB 3; Length 16;</p> <p>Best Local Similarity 100.0%; Pred. No. 0.00052;</p> <p>Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 11 RRPPLPPPLPPLPPI 26</p> <p> </p> <p>Db 1 RRPPLPPPLPPLPPI 16</p> <p>RESULT 15</p> <p>US-08-930-777A-5</p> <p>; Sequence 5, Application US/08930777A</p> <p>; Patent No. 6713605</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Blecha, Frank</p> <p>; APPLICANT: Shi, Jishu</p> <p>; TITLE OF INVENTION: Synthetic Antimicrobial Peptide</p> <p>; NUMBER OF SEQUENCES: 9</p> <p>; CORRESPONDENCE ADDRESS:</p> <p>; ADDRESSEE: Hovey, Williams, Timmons & Collins</p> <p>; STREET: 2405 Grand Blvd., Ste. 400</p> <p>; CITY: Kansas City</p> <p>; STATE: Missouri</p> <p>; COUNTRY: U.S.A.</p> <p>; ZIP: 64108</p> <p>; COMPUTER READABLE FORM:</p> <p>; MEDIUM TYPE: Floppy disk</p> <p>; COMPUTER: IBM PC compatible</p> <p>; OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>; SOFTWARE: PatentIn Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/930,777A</p> <p>FILING DATE: October 8, 1997</p> <p>CLASSIFICATION: 530</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: PCT/US96/04674</p> <p>FILING DATE: April 10, 1996</p> <p>NAME: COLLINS, JOHN M.</p> <p>REGISTRATION NUMBER: 26,262</p> <p>REFERENCE/DOCKET NUMBER: 23625-A</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (816) 474-9050</p> <p>TELEFAX: (816) 474-9057</p>


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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-930-777A-5

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Query Match 61.9%; Score 96; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db . 1 RPRPPPPPPRLPPRI 16

Search completed: October 26, 2005, 05:21:57
Job time : 27.7091 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 05:05:05 ; Search time 95.9636 Seconds
(without alignments)
113.119 Million cell updates/sec

Title: US-10-014-147-2

Perfect score: 155

Sequence: 1 RRRPPPLPRPPPPPPPPPPRLPPRI 26

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Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	155	100.0	26	15	US-10-651-147-2
3	155	100.0	38	9	US-09-738-742-1
4	155	100.0	38	9	US-09-739-535-1
5	155	100.0	39	14	US-10-014-147-1
6	155	100.0	39	15	US-10-391-155-1
7	155	100.0	39	15	US-10-391-155-2
8	155	100.0	39	15	US-10-391-155-6
9	155	100.0	39	15	US-10-651-147-1
10	155	100.0	42	16	US-10-344-709C-18
11	155	100.0	42	17	US-10-916-185-14

12	155	100.0	42	18	US-10-991-286A-44	Sequence 44, Appl
13	155	100.0	42	20	US-11-004-379-20	Sequence 20, Appl
14	140	90.3	23	14	US-10-014-147-3	Sequence 3, Appl
15	140	90.3	23	15	US-10-651-147-3	Sequence 3, Appl
16	116	74.8	19	14	US-10-014-147-4	Sequence 4, Appl
17	116	74.8	19	15	US-10-651-147-4	Sequence 4, Appl
18	96	61.9	16	14	US-10-014-147-5	Sequence 5, Appl
19	96	61.9	16	15	US-10-651-147-5	Sequence 5, Appl
20	91	58.7	91	16	US-10-425-115-200180	Sequence 200180,
21	90	58.1	15	15	US-10-391-155-3	Sequence 3, Appl
22	89.5	57.7	304	14	US-10-156-761-13550	Sequence 13550, A
23	86.5	55.8	200	16	US-10-425-115-206766	Sequence 206766,
24	84.5	54.5	322	16	US-10-425-115-316075	Sequence 316075,
25	84	54.2	182	16	US-10-425-115-232475	Sequence 232475,
26	83.5	53.9	245	16	US-10-425-115-206869	Sequence 206869,
27	83	53.5	14	14	US-10-014-147-7	Sequence 7, Appl
28	83	53.5	14	15	US-10-651-147-7	Sequence 7, Appl
29	83	53.5	86	16	US-10-437-963-131741	Sequence 131741,
30	83	53.5	192	16	US-10-437-963-143333	Sequence 143333,
31	82.5	53.2	276	16	US-10-437-963-132896	Sequence 132896,
32	82	52.9	59	9	US-09-030-619-163	Sequence 163, App
33	82	52.9	59	9	US-09-912-609-51	Sequence 51, Appl
34	82	52.9	59	15	US-10-277-232-163	Sequence 163, App
35	82	52.9	59	15	US-10-277-233-163	Sequence 163, App
36	82	52.9	59	17	US-10-838-289-683	Sequence 683, App
37	82	52.9	60	16	US-10-344-709C-17	Sequence 17, Appl
38	81.5	52.6	80	15	US-10-424-599-231660	Sequence 231660,
39	81.5	52.6	483	16	US-10-437-963-191498	Sequence 191498,
40	81	52.3	163	16	US-10-437-963-144892	Sequence 144892,
41	81	52.3	179	16	US-10-767-701-35404	Sequence 35404, A
42	80.5	51.9	255	16	US-10-425-115-316074	Sequence 316074,
43	80.5	51.9	284	16	US-10-425-115-316071	Sequence 316071,
44	80	51.6	109	15	US-10-424-599-267648	Sequence 267648,
45	80	51.6	132	16	US-10-767-701-51171	Sequence 51171, A

ALIGNMENTS

RESULT 1

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; Sequence 2, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A

RESULT 8

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; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: MODIFIED IRNA AGENTS
; FILE REFERENCE: 14174-091001
; CURRENT APPLICATION NUMBER: US/10/916,185
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US2004/011829
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/506,341
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 60/510,246
; PRIOR FILING DATE: 2003-10-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptides
; US-10-916-185-14

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Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RRRPPYLPRLPPPPPPPPPPRLPPRI 26

RESULT 12
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; Sequence 44, Application US/10991286A
; Publication No. US20050186591A1
; GENERAL INFORMATION:
; APPLICANT: Bumcrot, David
; APPLICANT: Farrer, Matthew J.
; APPLICANT: Maraganore, Demetrius M.
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: METHOD OF TREATING NEURODEGENERATIVE DISEASE
; FILE REFERENCE: 17574-003001
; CURRENT APPLICATION NUMBER: US/10/991,286A
; CURRENT FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: PCT/US2004/18271
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/476,947
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 42
; TYPE: PRT
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; OTHER INFORMATION: Exemplary Cell Permeation Peptide
; US-10-991-286A-44

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; Publication No. US2005015337A1
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; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: IRNA CONJUGATES
; FILE REFERENCE: 14174-067001
; CURRENT APPLICATION NUMBER: US/11/004,379
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: PCT/US04/10586
; PRIOR FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 60/460,783
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/462,894
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 63
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; SEQ ID NO 20
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptides
; US-11-004-379-20

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Best Local Similarity 100.0%; Pred. No. 1.2e-07;
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Db 1 RRRPPYLPRLPPPPPPPPPPRLPPRI 26

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; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
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ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/014,147
APPLICATION NUMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-014-147-3
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DB 1 PRPPYLPRPPPPPPPPPPRLPPRI 23
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Sequence 3, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-651-147-3
Query Match 90.3%; Score 140; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 PRPPYLPRPPPPPPPPPPRLPPRI 23
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Job time : 96.9636 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 04:51:43 ; Search time 62.9818 Seconds
(without alignments)
98.253 Million cell updates/sec

Title: US-10-014-147-5

Perfect score: 96
Sequence: 1 RRRPPPPPPRLPPRI 16

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Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqp19908:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038s:*

8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	16	2 AAW01448	Leukocyte
2	96	100.0	16	2 AAW75724	Proline/A
3	96	100.0	16	8 ADE86116	Proline-a
4	96	100.0	16	8 ADL67258	Antimicro
5	96	100.0	23	2 AAW01451	Leukocyte
6	96	100.0	23	8 ADE86114	Proline-a
7	96	100.0	23	8 ADL67256	Antimicro
8	96	100.0	26	2 AAW01447	Leukocyte
9	96	100.0	26	2 AAW75723	Proline/A
10	96	100.0	26	8 ADE86113	Proline-a
11	96	100.0	26	8 ADL67255	Antimicro
12	96	100.0	39	2 AAR30491	Antibacte
13	96	100.0	39	2 AAR99121	Magainin-
14	96	100.0	39	2 AAR94446	Synducin
15	96	100.0	39	2 AAW01446	Leukocyte
16	96	100.0	39	2 AAW75722	Proline/A
17	96	100.0	39	3 AAB36888	PR-39 pep
18	96	100.0	39	4 AAB97280	PR-39 pep
19	96	100.0	39	4 AAB84690	Amino aci
20	96	100.0	39	8 ADD35364	Antimicro
21	96	100.0	39	8 ADE86112	Proline-a
22	96	100.0	42	8 ADL67254	Antimicro
23	96	100.0	42	5 ABB07114	Antimicro
24	96	100.0	42	8 ADR82250	Cell perm
25	96	100.0	44	4 AAB51194	E. coli A

ALIGNMENTS

RESULT 1

AAW01448
ID AAW01448 standard; peptide; 16 AA.

XX AC AAW01448;

XX DT 18-JUN-1997 (first entry)

XX DE Leukocyte O2- production inhibitor peptide PR16.

XX KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
XX KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
XX KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
XX KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
XX KW tissue damage; oxygen radical; inflammatory disease; therapy.

XX OS Synthetic.

XX PN WO9632129-Al.

XX PD 17-OCT-1996.

XX PF 10-APR-1996; 96WO-US004674.

XX PR 10-APR-1995; 95US-00419066.

XX PA (UNIV) UNIV KANSAS STATE RES FOUND.

XX PI Blecha F, Shi J;

XX DR WPI; 1996-476842/47.

XX PT Inhibition of leukocyte superoxide anion prodn. and attraction of
XX PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.

XX PS Claim 12; Page 28; 45pp; English.

XX CC AAW01447-W01454 represent fragments of the proline-arginine rich
XX CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
XX CC isolated from porcine small intestine, and has also been identified in
XX CC human and porcine neutrophils. PR39 kills bacteria by interfering with
XX CC DNA and/or protein synthesis. PR39 also induces syndecan expression on
XX CC mesenchymal cells. Syndecans are important in wound repair, showing that
XX CC PR39 can be used in wound repair, as well as in antibacterial agents.
XX CC These sequences, and PR39, can be used in the method of the invention.
XX CC The method of the invention is for inhibiting leukocyte superoxide anion
XX CC (O2-) production. The method comprises administering to a leukocyte a
XX CC peptide (such as this sequence) capable of inhibiting leukocyte O2-

26 63 65.6 311 2 AAY17387 Aay17387 Human DNA
27 60 62.5 520 4 ABUS2849 Abu52849 Human ute
28 60 62.5 521 2 AAW74802 Aw74802 Human sec
29 60 62.5 521 5 ABG95252 Abg95252 Human nov
30 60 62.5 521 6 ABO34446 Abo34446 Region of
31 60 62.5 521 7 ADI23107 Adh74109 Novel hum
32 60 62.5 521 8 ADH74109 Adh74109 Human sec
33 60 62.5 526 3 AAB56895 Aab56895 Human pro
34 60 62.5 535 7 ADC31125 Adc31125 Human pro
35 60 62.5 565 4 AAM78694 Aam78694 Human pro
36 60 62.5 594 4 AAY72162 Aay72162 Human RNA
37 60 62.5 594 8 ADQ96576 Adq96576 T cell ac
38 59 61.5 209 4 AAU15847 Aau15847 Human nov
39 59 61.5 209 6 ABUS4916 Abu54916 Human nov
40 59 61.5 292 4 AAU16308 Aau16308 Human nov
41 59 61.5 292 6 ABUS5377 Abu55377 Human nov
42 59 61.5 313 2 AAY02613 Aay02613 Protein e
43 59 61.5 347 4 ABB50177 Abb50177 Human tra
44 59 61.5 347 7 ADB64690 Adb64690 Human pro
45 59 61.5 347 7 ADC31185 Adc31185 Human nov

CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting tissue
 CC damage at the wound site caused by excessive oxygen radicals produced by
 CC these leukocytes. They can also be used to develop products for treating
 CC inflammatory disease states
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 96; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPRPPPPPPRLPPRI 16
 |||||
 Db 1 RPRPPPPPPRLPPRI 16

RESULT 2
 AAW75724
 ID AAW75724 standard; peptide; 16 AA.

XX
 AC AAW75724;

DT 19-NOV-1998 (first entry)

DE Proline/Arginine rich peptide.

KW Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;
 KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;
 KW coronary bypass; organ transplantation surgery.

XX Synthetic.

XX WO9835690-A1.

PN 20-AUG-1998.

PF 17-FEB-1998; 98WO-US003207.

PR 18-FEB-1997; 97US-00802306.

PR 16-FEB-1998; 98US-00024975.

PA (UNIV) UNIV KANSAS STATE RES FOUND.

PI Ross CR, Blecha F, Shi J;

DR WPI; 1998-495359/42.

PT Reduction of reperfusion injury in temporarily occluded blood vessels -
 PT by administration of a peptide which is rich in proline or arginine
 PT residues.

PS Claim 3; Page 15; 35pp; English.

XX Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
 CC administration into a mammal's bloodstream reduce reperfusion injury
 CC (production of reactive oxygen species, neutrophil adherence to
 CC endothelium, and extravasation of neutrophils). These peptides have two
 CC requirements: they contain the consensus sequence PXXP, where P is a
 CC proline residue and X is any amino acid residue, which has been found to
 CC inhibit superoxide production, and secondly they have arginine residues
 CC adjacent to these motifs, required for effective inhibition. It was
 CC established by structural and function analysis that a peptide should
 CC ideally contain 4 or 6 of these motifs, and that inhibitory activity is
 CC correlated with the increase of length of peptides. The effectiveness of
 CC these peptides was determined by investigating the production of the
 CC neutrophil superoxide anion, and also the inhibition of neutrophil
 CC chemotaxis. From this, it was found that all of the peptides inhibited
 CC NADPH oxidase to some extent. All of the peptides also inhibit neutrophil
 CC oxidase activity. PR-39 is believed, to be the most potent endogenous
 CC down regulator of NADPH oxidase yet discovered, and from the data
 CC produced, it can be suggested to be involved in eliminating or reducing
 CC the reperfusion injury induced adhesion and extraction of neutrophils.

CC The peptides are also useful in connection with surgical procedures such
 CC as coronary bypass and organ transplantation surgery
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 96; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPRPPPPPPRLPPRI 16
 |||||
 Db 1 RPRPPPPPPRLPPRI 16

RESULT 3
 ADE86116
 ID ADE86116 standard; peptide; 16 AA.

XX
 AC ADE86116;

DT 29-JAN-2004 (first entry)

DE Proline-arginine (PR)-rich antimicrobial peptide PR-16.

KW Leukocyte superoxide anion; leukocyte O2- production;
 KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;
 KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;
 KW tissue damage; oxygen radical; antibacterial.

XX Synthetic.

XX US2003125249-A1.

PN 03-JUL-2003.

PF 07-DEC-2001; 2001US-00014147.

PR 10-APR-1995; 95US-00419066.

PR 08-OCT-1997; 97US-00930777.

PA (BLEC/) BLECHA F.

PA (SHIJ/) SHI J.

PI Blecha F, Shi J;

DR WPI; 2004-059188/06.

PT Attracting leukocyte to location by administering peptide including
 PT proline-arginine-rich antimicrobial peptide or its truncated analogs to
 PT the location.

PS Claim 3; SEQ ID NO 5; 24pp; English.

XX The present invention relates to a method of inhibiting leukocyte
 CC superoxide anion (O2-) production and/or attracting leukocytes. The
 CC method comprises the use of proline-arginine (PR)-rich antimicrobial
 CC peptides or their truncated analogues. The method is useful for
 CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or
 CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are
 CC useful as medicaments to fight infection by attracting leukocytes to a
 CC wound site, while restricting tissue damage at the wound site caused by
 CC excessive oxygen radicals produced by these leukocytes. The present
 CC sequence represents a PR-rich antimicrobial peptide.

XX Sequence 16 AA;

Query Match 100.0%; Score 96; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPRPPPPPPRLPPRI 16
 |||||
 Db 1 RPRPPPPPPRLPPRI 16

RESULT 4
 ADL67258
 ID ADL67258 standard; peptide; 16 AA.
 AC ADL67258;
 XX
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Antimicrobial peptide PR-39 analog PR-16.
 XX
 KW Leucocyte; superoxide anion; oxygen radical; proline-arginine;
 KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;
 KW infection; wound; tissue damage; PR-39 analog; PR-16.
 XX
 OS Unidentified.
 XX
 XX US2004043934-A1.
 PN
 XX
 PD 04-MAR-2004.
 XX
 XX 28-AUG-2003; 2003US-00651147.
 XX
 PF 10-APR-1995; 95US-00419066.
 PR
 PR 08-OCT-1997; 97US-00930777.
 XX
 XX (BLEC/) BLECHA F.
 PA (SHIJ/) SHI J.
 XX
 PI Blecha F, Shi J;
 XX
 XX WPI; 2004-225728/21.
 DR
 XX
 XX Inhibiting leukocyte oxygen radical production comprises contacting a
 PT leukocyte with a peptide, where the inhibition occurs as a consequence of
 PT binding between the peptide and p47phox.
 XX
 XX Claim 9; SEQ ID NO 5; 24pp; English.
 XX
 CC The invention relates to inhibiting leukocyte superoxide anion (O2-)
 CC production using a naturally occurring proline-arginine (PR)-rich
 CC antimicrobial peptide known as PR-39 and its truncated analogs. The
 CC method comprises contacting leukocytes with the peptide comprising 39 or
 CC 26 amino acids, for a time and under conditions effective to inhibit
 CC of NADPH oxidase anion production. The peptide inhibits the activity
 CC of NADPH oxidase responsible for anion production, by binding to Src
 CC homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein
 CC of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or
 CC porcine leukocyte and the mammalian leukocyte is neutrophil. Another
 CC method is also disclosed which employs a PR-39 analog that comprise 16
 CC amino acids, where the sum of the proline and arginine residues in the
 CC effective peptide is at least 66 or 74 % of the total number of amino
 CC acids. This peptide inhibits leukocyte O2- production by the effective
 CC binding to p47phox in whole cells, therefore interfering with the binding
 CC of p47phox to p22phox. At least 14 or 25% of the amino acid residues in
 CC the peptide are arginine residues. The method of the invention is useful
 CC for inhibiting leukocyte oxygen radical production. The peptides are
 CC useful as medicaments for fighting infections by attracting leukocytes to
 CC a wound site, yet restrict tissue damage at the wound site caused by
 CC excessive oxygen radicals produced by these leukocytes. The present
 CC sequence is PR-39 analog, PR-16.
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 100.0%; Score 96; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. NO. 0.00017;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRPFPFPFPRLPPRI 16
 |||||
 DB 1 RRPFPFPFPRLPPRI 16
 |||||

RESULT 5
 AAW01451
 ID AAW01451 standard; peptide; 23 AA.
 AC AAW01451;
 XX
 XX 18-JUN-1997 (first entry)
 DT
 DE Leucocyte O2- production inhibitor peptide PR23.
 XX
 KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
 KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 KW tissue damage; oxygen radical; inflammatory disease; therapy.
 XX
 OS Synthetic.
 XX
 XX WO9632129-A1.
 PN
 XX
 PD 17-OCT-1996.
 XX
 PF 10-APR-1996; 96WO-US004674.
 PR
 PR 10-APR-1995; 95US-00419066.
 XX
 XX (UNIV) UNIV KANSAS STATE RES FOUND.
 PA
 XX Blecha F, Shi J;
 PI
 XX WPI; 1996-476842/47.
 DR
 XX
 XX Inhibition of leukocyte superoxide anion prodn. and attraction of
 PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.
 PT
 XX Disclosure; Page 27; 45pp; English.
 PS
 XX
 CC AAW01447-W01454 represent fragments of the proline-arginine rich
 CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
 CC isolated from porcine small intestine, and has also been identified in
 CC human and porcine neutrophils. PR39 kills bacteria by interfering with
 CC DNA and/or protein synthesis. PR39 also induces syndecan expression on
 CC mesenchymal cells. Syndecans are important in wound repair, showing that
 CC PR39 can be used in wound repair, as well as in antibacterial agents.
 CC These sequences, and PR39, can be used in the method of the invention.
 CC The method of the invention is for inhibiting leukocyte superoxide anion
 CC (O2-) production. The method comprises administering to a leukocyte a
 CC peptide (such as this sequence) capable of inhibiting leukocyte O2-
 CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting tissue
 CC damage at the wound site caused by excessive oxygen radicals produced by
 CC these leukocytes. They can also be used to develop products for treating
 CC inflammatory disease states
 XX
 XX Sequence 23 AA;
 SQ
 Query Match 100.0%; Score 96; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. NO. 0.00023;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRPFPFPFPRLPPRI 16
 |||||
 DB 8 RRPFPFPFPRLPPRI 23
 |||||

RESULT 6
 ADE86114
 ID ADE86114 standard; peptide; 23 AA.
 AC ADE86114;
 XX
 XX 29-JAN-2004 (first entry)
 DT

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XX DE Proline-arginine (PR)-rich antimicrobial peptide PR-23.
XX KW Leukocyte superoxide anion; leukocyte O2- production;
XX KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;
XX KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;
XX KW tissue damage; oxygen radical; antibacterial.
XX OS Synthetic.
XX PN US2003125249-A1.
XX PD 03-JUL-2003.
XX PF 07-DEC-2001; 2001US-00014147.
XX PR 10-APR-1995; 95US-00419066.
XX PR 08-OCT-1997; 97US-00930777.
XX PA (BLEC/) BLECHA F.
XX PA (SHIJ/) SHI J.
XX PI Blecha F, Shi J;
XX DR WPI; 2004-059188/06.
XX XX Attracting leukocyte to location by administering peptide including
XX PT proline-arginine-rich antimicrobial peptide or its truncated analogs to
XX PT the location.
XX PS Example; SEQ ID NO 3; 24pp; English.
XX CC The present invention relates to a method of inhibiting leukocyte
XX CC superoxide anion (O2-) production and/or attracting leukocytes. The
XX CC method comprises the use of proline-arginine (PR)-rich antimicrobial
XX CC peptides or their truncated analogues. The method is useful for
XX CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or
XX CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are
XX CC useful as medicaments to fight infection by attracting leukocytes to a
XX CC wound site, while restricting tissue damage at the wound site caused by
XX CC excessive oxygen radicals produced by these leukocytes. The present
XX CC sequence represents a PR-rich antimicrobial peptide.
XX SQ Sequence 23 AA;
XX Query Match 100.0%; Score 96; DB 8; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 0.00023;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 RRPDPFPFPPRLPPRI 16
XX DB ||||| ||||| ||||| |||||
XX 8 RRPDPFPFPPRLPPRI 23
XX RESULT 7
XX ADL67256
XX ID ADL67256 standard; peptide; 23 AA.
XX AC ADL67256;
XX XX 20-MAY-2004 (first entry)
XX DT Antimicrobial peptide PR-39 analog PR-23.
XX DE Leukocyte; superoxide anion; oxygen radical; proline-arginine;
XX KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;
XX KW infection; wound; tissue damage; PR-39 analog; PR-23.
XX OS Unidentified.
XX PN US2004043934-A1.
XX PD 04-MAR-2004.
XX PF 28-AUG-2003; 2003US-00651147.
XX PR 10-APR-1995; 95US-00419066.
XX PR 08-OCT-1997; 97US-00930777.
XX PA (BLEC/) BLECHA F.
XX PA (SHIJ/) SHI J.
XX PI Blecha F, Shi J;
XX DR WPI; 2004-225728/21.
XX XX Inhibiting leukocyte oxygen radical production comprises contacting a
XX PT leukocyte with a peptide, where the inhibition occurs as a consequence of
XX PT binding between the peptide and p47phox.
XX PS Example; SEQ ID NO 3; 24pp; English.
XX CC The invention relates to inhibiting leukocyte superoxide anion (O2-)
XX CC production using a naturally occurring proline-arginine (PR)-rich
XX CC antimicrobial peptide known as PR-39 and its truncated analogs. The
XX CC method comprises contacting leukocytes with the peptide comprising 39 or
XX CC 26 amino acids, for a time and under conditions effective to inhibit
XX CC leukocyte superoxide anion production. The peptide inhibits the activity
XX CC of NADPH oxidase responsible for anion production, by binding to Src
XX CC homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein
XX CC of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or
XX CC porcine leukocyte and the mammalian leukocyte is neutrophil. Another
XX CC method is also disclosed which employs a PR-39 analog that comprise 16
XX CC amino acids, where the sum of the proline and arginine residues in the
XX CC effective peptide is at least 66 or 74 % of the total number of amino
XX CC acids. This peptide inhibits leukocyte O2- production by the effective
XX CC binding to p47phox in whole cells, therefore interfering with the binding
XX CC of p47phox to p22phox. At least 14 or 25% of the amino acid residues in
XX CC the peptide are arginine residues. The method of the invention is useful
XX CC for inhibiting leukocyte oxygen radical production. The peptides are
XX CC useful as medicaments for fighting infections by attracting leukocytes to
XX CC a wound site, yet restrict tissue damage at the wound site caused by
XX CC excessive oxygen radicals produced by these leukocytes. The present
XX CC sequence is PR-39 analog, PR-23.
XX SQ Sequence 23 AA;
XX Query Match 100.0%; Score 96; DB 8; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 0.00023;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 RRPDPFPFPPRLPPRI 16
XX DB ||||| ||||| ||||| |||||
XX 8 RRPDPFPFPPRLPPRI 23
XX RESULT 8
XX AAW01447
XX ID AAW01447 standard; peptide; 26 AA.
XX AC AAW01447;
XX XX 18-JUN-1997 (first entry)
XX DT Leukocyte O2- production inhibitor peptide PR26.
XX DE Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
XX KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
XX KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
XX KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
XX KW tissue damage; oxygen radical; inflammatory disease; therapy.
XX OS Synthetic.
XX PN WO9632129-A1.

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PD 17-OCT-1996.
 XX
 PF 10-APR-1996; 96WO-US004674.
 XX
 PR 10-APR-1995; 95US-00419066.
 XX
 PA (UNIV) UNIV KANSAS STATE RES FOUND.
 XX
 PI Blecha F, Shi J;
 XX
 DR WPI; 1996-476842/47.
 XX
 PT Inhibition of leukocyte superoxide anion prodn. and attraction of
 PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.
 XX
 PS Claim 3; Page 26; 45pp; English.
 XX
 CC AAW01447-W01454 represent fragments of the proline-arginine rich
 CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
 CC isolated from porcine small intestine, and has also been identified in
 CC human and porcine neutrophils. PR39 kills bacteria by interfering with
 CC DNA and/or protein synthesis. PR39 also induces syndecan expression on
 CC mesenchymal cells. Syndecans are important in wound repair, showing that
 CC PR39 can be used in wound repair, as well as in antibacterial agents.
 CC These sequences, and PR39, can be used in the method of the invention.
 CC The method of the invention is for inhibiting leukocyte superoxide anion
 CC (O2-) production. The method comprises administering to a leukocyte a
 CC peptide (such as this sequence) capable of inhibiting leukocyte O2-
 CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting tissue
 CC damage at the wound site caused by excessive oxygen radicals produced by
 CC these leukocytes. They can also be used to develop products for treating
 CC inflammatory disease states
 XX
 SQ Sequence 26 AA;
 Query Match 100.0%; Score 96; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00026;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRPDPDPDPDPRLPPRI 16
 |||||
 DB 11 RRPDPDPDPDPRLPPRI 26
 |||||
 RESULT 9
 AAW75723
 ID AAW75723 standard; peptide; 26 AA.
 XX
 AC AAW75723;
 XX
 DT 19-NOV-1998 (first entry)
 XX
 DE Proline/Arginine rich peptide PR-26.
 XX
 KW Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;
 KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;
 KW coronary bypass; organ transplantation surgery.
 XX
 OS Synthetic.
 XX
 PN WO9835690-A1.
 XX
 PD 20-AUG-1998.
 XX
 PF 17-FEB-1998; 98WO-US003207.
 XX
 PR 18-FEB-1997; 97US-00802306.
 PR 16-FEB-1998; 98US-00024975.
 XX
 PA (UNIV) UNIV KANSAS STATE RES FOUND.
 XX
 PI Ross CR, Blecha F, Shi J;
 XX
 WPI; 1998-495359/42.
 Reduction of reperfusion injury in temporarily occluded blood vessels -
 by administration of a peptide which is rich in proline or arginine
 residues.
 Claim 3; Page 14-15; 35pp; English.
 Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
 administration into a mammal's bloodstream reduce reperfusion injury
 (production of reactive oxygen species, neutrophil adherence to
 endothelium, and extravasation of neutrophils). These peptides have two
 requirements: they contain the consensus sequence PXXP, where P is a
 proline residue and X is any amino acid residue, which has been found to
 inhibit superoxide production, and secondly they have arginine residues
 adjacent to these motifs, required for effective inhibition. It was
 established by structural and function analysis that a peptide should
 ideally contain 4 or 6 of these motifs, and that inhibitory activity is
 correlated with the increase of length of peptides. The effectiveness of
 these peptides was determined by investigating the production of the
 neutrophil superoxide anion, and also the inhibition of neutrophil
 chemotaxis. From this, it was found that all of the peptides inhibited
 NADPH oxidase to some extent. All of the peptides also inhibit neutrophil
 oxidase activity. PR-39 is believed, to be the most potent endogenous
 down regulator of NADPH oxidase yet discovered, and from the data
 produced, it can be suggested to be involved in eliminating or reducing
 the reperfusion injury induced adhesion and extraction of neutrophils.
 The peptides are also useful in connection with surgical procedures such
 as coronary bypass and organ transplantation surgery
 Sequence 26 AA;
 Query Match 100.0%; Score 96; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00026;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRPDPDPDPDPRLPPRI 16
 |||||
 DB 11 RRPDPDPDPDPRLPPRI 26
 |||||
 RESULT 10
 ADE86113
 ID ADE86113 standard; peptide; 26 AA.
 XX
 AC ADE86113;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Proline-arginine (PR)-rich antimicrobial peptide PR-26.
 XX
 KW Leukocyte superoxide anion; leukocyte O2- production;
 KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;
 KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;
 KW tissue damage; oxygen radical; antibacterial.
 XX
 OS Synthetic.
 XX
 PN US2003125249-A1.
 XX
 PD 03-JUL-2003.
 XX
 PF 07-DEC-2001; 2001US-00014147.
 XX
 PR 10-APR-1995; 95US-00419066.
 PR 08-OCT-1997; 97US-00930777.
 XX
 PA (BLEC/) BLECHA F.
 PA (SHIJ/) SHI J.
 XX
 PI Blecha F, Shi J;
 XX

DR WPI; 2004-059188/06.
 XX Attracting leukocyte to location by administering peptide including
 PT proline-arginine-rich antimicrobial peptide or its truncated analogs to
 PT the location.
 XX
 PS Claim 3; SEQ ID NO 2; 24pp; English.
 XX
 CC The present invention relates to a method of inhibiting leukocyte
 CC superoxide anion (O₂⁻) production and/or attracting leukocytes. The
 CC method comprises the use of proline-arginine (PR)-rich antimicrobial
 CC peptides or their truncated analogues. The method is useful for
 CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or
 CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are
 CC useful as medicaments to fight infection by attracting leukocytes to a
 CC wound site, while restricting tissue damage at the wound site caused by
 CC excessive oxygen radicals produced by these leukocytes. The present
 CC sequence represents a PR-rich antimicrobial peptide.
 XX
 SQ Sequence 26 AA;
 Query Match 100.0%; Score 96; DB 8; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00026;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RPRPPPPPPRLPPRI 16
 Db 11 RPRPPPPPPRLPPRI 26
 ADL67255
 ID ADL67255 standard; peptide; 26 AA.
 AC ADL67255;
 XX
 XX 20-MAY-2004 (first entry)
 DE Antimicrobial peptide PR-39 analog PR-26.
 XX
 KW Leucocyte; superoxide anion; oxygen radical; proline-arginine;
 KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;
 KW infection; wound; tissue damage; PR-39 analog; PR-26.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Region 1..3
 FT /note= "Essential for antibacterial activity"
 FT Region 20..26
 FT /note= "Essential for antibacterial activity"
 XX
 PN US2004043934-A1.
 XX
 PD 04-MAR-2004.
 XX
 PF 28-AUG-2003; 2003US-00651147.
 XX
 PR 10-APR-1995; 95US-00419066.
 PR 08-OCT-1997; 97US-00930777.
 XX
 XX (BLEC/) BLECHA F.
 PA (SHIJ/) SHI J.
 XX
 XX Blecha F, Shi J;
 XX
 XX WPI; 2004-225728/21.
 DR
 XX Inhibiting leukocyte oxygen radical production comprises contacting a
 PT leukocyte with a peptide, where the inhibition occurs as a consequence of
 PT binding between the peptide and p47phox.
 XX
 PS Claim 1; SEQ ID NO 2; 24pp; English.

XX The invention relates to inhibiting leukocyte superoxide anion (O₂⁻)
 CC production using a naturally occurring proline-arginine (PR)-rich
 CC antimicrobial peptide known as PR-39 and its truncated analogs. The
 CC method comprises contacting leukocytes with the peptide comprising 39 or
 CC 26 amino acids, for a time and under conditions effective to inhibit
 CC leukocyte superoxide anion production. The peptide inhibits the activity
 CC of NADPH oxidase responsible for anion production, by binding to Src
 CC homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein
 CC of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or
 CC porcine leukocyte and the mammalian leukocyte is neutrophil. Another
 CC method is also disclosed which employs a PR-39 analog that comprise 16
 CC amino acids, where the sum of the proline and arginine residues in the
 CC effective peptide is at least 66 or 74 % of the total number of amino
 CC acids. This peptide inhibits leukocyte O₂⁻ production by the effective
 CC binding to p47phox in whole cells, therefore interfering with the binding
 CC of p47phox to p22phox. At least 14 or 25% of the amino acid residues in
 CC the peptide are arginine residues. The method of the invention is useful
 CC for inhibiting leukocyte oxygen radical production. The peptides are
 CC useful as medicaments for fighting infections by attracting leukocytes to
 CC a wound site, yet restrict tissue damage at the wound site caused by
 CC excessive oxygen radicals produced by these leukocytes. The present
 CC sequence is PR-39 analog PR-26.
 XX
 SQ Sequence 26 AA;
 Query Match 100.0%; Score 96; DB 8; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00026;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RPRPPPPPPRLPPRI 16
 Db 11 RPRPPPPPPRLPPRI 26
 AAR30491
 ID AAR30491 standard; peptide; 39 AA.
 XX
 AC AAR30491;
 XX
 XX 25-MAR-2003 (revised)
 DT 12-MAY-1993 (first entry)
 XX
 XX Antibacterial peptide.
 DE
 XX
 KW Pig; small intestine; endocrine; gram negative; bacteria; therapeutic;
 KW veterinary medicine; prophylactic.
 XX
 OS Sus scrofa domestica.
 XX
 PN WO9222578-A1.
 XX
 PD 23-DEC-1992.
 XX
 PF 10-JUN-1992; 92WO-SE000394.
 XX
 PR 14-JUN-1991; 91SE-00001838.
 XX
 XX (LEEJ/) LEE J.
 PA (BOMA/) BOMAN H G.
 PA (MUTT/) MUTT V.
 PA (JOER/) JOERNVALL H.
 XX
 PI Lee J, Boman HG, Mutt V, Joernvall H;
 XX
 XX WPI; 1993-018080/02.
 DR
 XX New anti-bacterial polypeptide - active against Gram negative bacteria.
 PT
 XX Claim 1; Page 10; 15pp; English.
 PS
 XX This peptide was isolated from the small intestine of a pig. The small

CC inestine is an important endocrine organ and many physiologically active
 CC peptides have been isolated from it. This peptide inhibits the growth of,
 CC and may kill, bacteria, pref. gram negative bacteria. This peptide or its
 CC functional derivatives may be used in human or veterinary medicine for
 CC therapeutic or prophylactic use. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ

Sequence 39 AA;

Query Match 100.0%; Score 96; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPPPRLPPRI 16
 |||||
 DB 11 RPRPPPPPPRLPPRI 26

RESULT 13
 AAR99121
 ID AAR99121 standard; peptide; 39 AA.

AC AAR99121;

DT 28-OCT-1996 (first entry)

XX Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.

XX STD; sexually transmitted disease; HIV; human immunodeficiency virus;
 KW herpes simplex virus; HSV; Neisseria gonorrhoeae; Candida; Chlamydia;
 KW magainin; antimicrobial; squalamine.

XX Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 39
 FT /note= "amidated"

XX W09608270-A2.

XX 21-MAR-1996.

XX 13-SEP-1995; 95WO-US011675.

XX 13-SEP-1994; 94US-00305475.

XX (MAGA-) MAGAININ PHARM INC.

XX Jacob L, Zasloff M, Williams T, Bedi G;

XX WPI; 1996-179725/18.

XX Inhibiting sexually transmitted disease e.g. HIV or herpes simplex - by
 PT administering magainin antimicrobial or squalamine cpd. to inhibit
 PT transmission.

XX Example 1; Page 32; 60pp; English.

XX AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may be
 CC used to treat sexually transmitted diseases (STDs) caused by Chlamydia,
 CC HIV, herpes simplex virus, Neisseria gonorrhoeae or Candida infection.
 CC The peptides inhibit STDs by either killing the infectious organism,
 CC impeding the infection mechanism or interrupting the replication cycle of
 CC the organism. Squalamine (an aminosterol host defence molecule of the dog
 CC fish shark Squalus acanthias) and PGla (a frog antimicrobial peptide)
 CC analogues may also be useful in inhibiting STD infection and transmission

XX Sequence 39 AA;

Query Match 100.0%; Score 96; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPPPRLPPRI 16
 |||||
 DB 11 RPRPPPPPPRLPPRI 26

RESULT 14

AAR94446
 ID AAR94446 standard; peptide; 39 AA.

XX AAR94446;

XX 05-NOV-1996 (first entry)

XX Synducin peptide (PR-39) induces syndecan expression.

XX Synducin; induction; expression; syndecan-1; syndecan-4; surface;
 KW mesenchymal cell; fibroblast; epithelial; PR-39; treatment; stasis;
 KW decubitus; ulcers; keloids; skin burns; ischemic tissues;
 KW hypercoagulation states; prevention; tumour metastasis; restenosis;
 KW inhibition; angiogenesis; proliferation; endothelial.

XX Synthetic.

XX W09609322-A2.

XX 28-MAR-1996.

XX 22-SEP-1995; 95WO-US012080.

XX 22-SEP-1994; 94US-00310722.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Gallo RL, Bernfield M;

XX WPI; 1996-188401/19.

XX Modulating mesenchymal interaction by administration of synducin - used
 PT in the treatment of wounds, tumours, restenosis, etc.

XX Claim 4; Page 26; 34pp; English.

XX The present peptide is a synducin, which induces the expression of
 CC syndecan-1 and syndecan-4 on the surface of mesenchymal cells, esp.
 CC fibroblasts and epithelial cells. The 36 N-terminal amino acids of the
 CC peptide were found to be identical to the 36 N-terminal amino acids of PR
 CC -39, a pro and Arg rich antibacterial peptide previously found in porcine
 CC intestine (W09222578). Synducins may be used in the treatment of stasis
 CC and decubitus ulcers, keloids, skin burns, ischemic tissues and
 CC hypercoagulation states, prevention of tumour metastasis, restenosis
 CC inhibition and endothelial cell angiogenesis and proliferation induction.
 CC Human microvascular endothelial cells were assayed for syndecan-4
 CC expression following exposure to 5% wound fluid, dbcAMP (1 mM), the
 CC present peptide (10 microm) or a blank, to give respective cell surface
 CC syndecan-4 values (mOD/m in) of approx. 1.75, 1.70, 1.80 and 0.95

XX Sequence 39 AA;

Query Match 100.0%; Score 96; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPPPRLPPRI 16
 |||||
 DB 11 RPRPPPPPPRLPPRI 26

RESULT 15

AAR01446
 ID AAR01446 standard; peptide; 39 AA.

XX AAR01446;

XX

DT 18-JUN-1997 (first entry)
XX
DE Leukocyte O2- production inhibitor peptide PR39.
XX
KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
KW tissue damage; oxygen radical; inflammatory disease; therapy.
XX
OS Synthetic.
XX
PN WO9632129-A1.
XX
PD 17-OCT-1996.
XX
PF 10-APR-1996; 96WO-US004674.
XX
PR 10-APR-1995; 95US-00419066.
XX
PA (UNIV) UNIV KANSAS STATE RES FOUND.
XX
PI Blecha F, Shi J;
XX
XX WPI; 1996-476842/47.
XX
PT Inhibition of leukocyte super:oxide anion prodn. and attraction of
PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.
XX
PS Claim 2; Page 26; 45pp; English.
XX
CC This sequence represents the proline-arginine rich antimicrobial peptide
CC PR39. The PR39 sequence was first isolated from porcine small intestine,
CC and has also been identified in human and porcine neutrophils. PR39 kills
CC bacteria by interfering with DNA and/or protein synthesis. PR39 also
CC induces syndecan expression on mesenchymal cells. Syndecans are important
CC in wound repair, showing that PR39 can be used in wound repair, as well
CC as in antibacterial agents. This sequence, and the fragments of it shown
CC in AA01447-W01454, can be used in the method of the invention. The
CC method of the invention is for inhibiting leukocyte superoxide anion (O2-
CC) production. The method comprises administering to a leukocyte a peptide
CC (such as this sequence) capable of inhibiting leukocyte O2- production.
CC The peptides can be used as medicaments for fighting infection by
CC attracting leukocytes to a wound site and restricting tissue damage at
CC the wound site caused by excessive oxygen radicals produced by these
CC leukocytes. They can also be used to develop products for treating
CC inflammatory disease states
XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 96; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. NO. 0.00037;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPPPPPPRLPPRI 16
DB 11 RRRPPPPPPRLPPRI 26

Search completed: October 26, 2005, 05:12:07
Job time : 65.9818 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:00:14 ; Search time 11.9273 Seconds
(without alignments)
129.071 Million cell updates/sec

Title: US-10-014-147-5
Perfect score: 96
Sequence: 1 RRPAPPPPPRLPPRI 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	172	2 S68232	antimicrobial prot
2	61	63.5	301	2 JQ1663	hybrid proline-ric
3	59	61.5	2584	2 T24158	hypothetical prote
4	59	61.5	2606	2 T24157	hypothetical prote
5	58	60.4	212	2 S57330	cathelin-like anti
6	58	60.4	228	2 S40463	prophenin (PF-2) p
7	56.5	58.9	1137	2 A33507	hypothetical prote
8	56	58.3	736	2 I51691	dishevelled homolo
9	55.5	57.8	1029	2 T30351	mucin-like protein
10	55	57.3	164	2 T26608	hypothetical prote
11	55	57.3	227	2 C69432	hypothetical prote
12	55	57.3	716	2 T26998	hypothetical prote
13	55	57.3	2871	2 A55624	fibritin-1 precur
14	54	56.2	213	2 T48490	embryo-specific pr
15	54	56.2	302	2 TPCHTC	troponin T, cardia
16	54	56.2	540	2 B47417	insulin receptor-x
17	53	55.2	276	2 B25345	troponin T, cardia
18	53	55.2	276	2 A25345	troponin T, cardia
19	53	55.2	284	2 A28008	troponin T, cardia
20	53	55.2	306	2 I46903	troponin T, cardia
21	53	55.2	588	2 T45564	hypothetical prote
22	53	55.2	903	2 T00074	hypothetical prote
23	52.5	54.7	134	2 D84672	hypothetical prote
24	52	54.2	57	2 S10782	salivary protein p
25	52	54.2	79	1 PUHUSB	proline-rich pepti
26	52	54.2	134	2 JC5572	proline-rich prote
27	52	54.2	199	2 S14981	extensin class I (
28	52	54.2	215	2 S34163	homeotic protein H
29	52	54.2	305	2 JC4525	nucleic acid-bind

cytokinin-induced
RNA/DNA-binding pr
proline-rich prote
homeotic protein H
homeotic protein H
homeotic tyrosine k
probable nuclear a
hypothetical prote
spore coat protein
infected cell prot
hypothetical prote
cell wall protein
cell ligand - rat
proline-rich prote
extensin - Volvox
F44B9.3 protein -

ALIGNMENTS

RESULT 1

S68232
antimicrobial protein PR-39 precursor, cathelin-associated - pig
N:Alternate names: myeloid antibacterial protein PR-39
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S68232; JN0899; I47138; S19563
R/Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 376, 130-134, 1995
A:Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni
A/Reference number: S68232; MUID:96105365; PMID:7498526
A/Accession: S68232
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-172 <ZHA>
A/Cross-references: UNIPROT:P80054; EMBL:X89201; NID:gl165150; PIDN:CAA61487.1; PID:gl116;
A/Experimental source: leukocytes
R/Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
A:Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the i
A/Reference number: JN0899; MUID:94071853; PMID:8250863
A/Accession: JN0899
A/Molecule type: mRNA
A/Residues: 1-20, 'A', 22-172 <STO>
A/Cross-references: GB:I23825; NID:9435100; PIDN:AAA31109.1; PID:G435101
A/Experimental source: bone marrow cells
R/Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bone
Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
A:Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fami
A/Reference number: I47138; MUID:95350216; PMID:7624374
A/Accession: I47138
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-28, 'T', 30-89, 'OR', 92-116, 'NDP', 120-172 <GUD>
A/Cross-references: EMBL:X87236; NID:9829142; PIDN:CAA60682.1; PID:gl051298
R/Agarberth, B.; Lee, J.Y.; Bergman, I.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall,
Eur. J. Biochem. 202, 849-854, 1991
A:Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of t
A/Reference number: S19563; MUID:92111534; PMID:1765098
A/Accession: S19563
A/Molecule type: protein
A/Residues: 131-169 <AGE>
A/Experimental source: intestine
C/Genetics:
A/Gene: PR39
A/Introns: 66/3; 102/3; 126/3
C/Superfamily: cathelin; cystatin homology
C/Keywords: amidated carboxyl end; antibacterial
F:1-29/Domain: signal sequence #status predicted <SIG>
F:22-129/Domain: cystatin homology <CYS>
F:30-130/Domain: propeptide #status predicted <PRO>
F:131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>

F169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

Query Match 100.0%; Score 96; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPDPFPFPPRLPPRI 16
|||||
DB 141 RRPDPFPFPPRLPPRI 156

RESULT 2

JQ1663 hybrid proline-rich protein - maize

C:Species: Zea mays (maize)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JQ1663
R:Jose-Estanyol, M.; Ruiz-Avila, L.; Puigdomenech, P.

Plant Cell 4, 413-423, 1992
A:Title: A maize embryo-specific gene encodes a proline-rich and hydrophobic protein.
A:Reference number: JQ1663; MUID:92361259; PMID:1498600

A:Accession: JQ1663

A:Molecule type: DNA

A:Residues: 1-301 <WIL>

A:Cross-references: UNIPROT:Q41848; EMBL:X60432; NID:G433706; PIDN:CAA42959.1; PID:G4337

A:Experimental source: strain W64A

C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 63.5%; Score 61; DB 2; Length 301;
Best Local Similarity 64.3%; Pred. No. 1.7;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRPDPFPFPPRLPP 14
|||
DB 179 RSPDPYVPVPP 192

RESULT 3

T24158 hypothetical protein R11A8.7b - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T24158; T24179

R:Bardill, S.

submitted to the EMBL Data Library, April 1996

A:Reference number: Z19846

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Accession: T24158

A:Molecule type: DNA

A:Residues: 1-2584 <WIL>

A:Cross-references: UNIPROT:Q9TW88; EMBL:Z70686; PIDN:CAB54289.1; GSPDB:GN00022; CESP:R1

A:Experimental source: clone R10H10

R:Cummings, P.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19849

A:Accession: T24179

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2584 <WIL>

A:Cross-references: EMBL:Z70310; PIDN:CAB54294.1; GSPDB:GN00022; CESP:R11A8.7b

A:Experimental source: clone R11A8

C:Genetics:

A:Gene: CESP:R11A8.7b

A:Map position: 4

A:Introns: 24/3; 80/3; 137/2; 177/1; 218/3; 348/3; 507/2; 709/3; 753/2; 924/1; 1020/3; 1

Query Match 61.5%; Score 59; DB 2; Length 2584;
Best Local Similarity 64.3%; Pred. No. 24;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRPDPFPFPPRLPP 14
|||
DB 2499 RQPPFPVAPQAPP 2512

RESULT 4

T24157

hypothetical protein R11A8.7a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T24157; T24177

R:Bardill, S.

submitted to the EMBL Data Library, April 1996

A:Reference number: Z19846

A:Accession: T24157

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2606 <WIL>

A:Cross-references: UNIPROT:Q21920; EMBL:Z70686; PIDN:CAA94615.1; GSPDB:GN00022; CESP:R11

A:Experimental source: clone R10H10

R:Cummings, P.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19849

A:Accession: T24177

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2606 <WIL>

A:Cross-references: EMBL:Z70310; PIDN:CAA94370.1; GSPDB:GN00022; CESP:R11A8.7a

A:Experimental source: clone R11A8

C:Genetics:

A:Gene: CESP:R11A8.7a

A:Map position: 4

A:Introns: 24/3; 80/3; 137/2; 177/1; 218/3; 348/3; 507/2; 709/3; 753/2; 924/1; 1020/3; 1

Query Match 61.5%; Score 59; DB 2; Length 2606;

Best Local Similarity 64.3%; Pred. No. 25;

Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRPDPFPFPPRLPP 14

|||
DB 2521 RQPPFPVAPQAPP 2534

RESULT 5

S57330

cathelin-like antibacterial peptide precursor (clone C6) - pig (fragment)

N:Alternate names: antimicrobial peptide; prophenin-1

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: S57330; S68726

R:Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V.

Biol. Chem. Hoppe-Seyler 376, 507-510, 1995

A:Title: Molecular cloning and identification of a novel porcine cathelin-like antibacter

A:Reference number: S57330; MUID:96042752; PMID:7576250

A:Accession: S57330

A:Molecule type: mRNA

A:Residues: 1-212 <STR>

A:Cross-references: UNIPROT:P51524; GB:X86031; NID:g1006756; PIDN:CAA60023.1; PID:g100675

R:Harwig, S.S.L.; Kokryakov, V.N.; Swiderrek, K.M.; Aleshina, G.M.; Zhao, C.; Lehrer, R.I.

FEBS Lett. 362, 65-69, 1995

A:Title: Prophenin-1, an exceptionally proline-rich antimicrobial peptide from porcine le

A:Reference number: S68726; MUID:95212585; PMID:7698355

A:Accession: S68726

A:Molecule type: protein

A:Residues: 131-209 <HAR>

A:Experimental source: leukocytes

C:Superfamily: cathelin; cystatin homology

C:Keywords: antibacterial

F:6-113/Domain: cystatin homology <CYS>

Query Match 60.4%; Score 58; DB 2; Length 212;

Best Local Similarity 76.9%; Pred. No. 2.7;

Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 RPPFPFPPRLPP 15

|||||

Db 199 RPPFPGRPPR 211

RESULT 6

S40463
 prophenin (PF-2) precursor - pig
 N:Alternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S40463; S57331; S68233
 R:Pungercar, J.; Strukelj, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, F.; Turk, P.
 PFBs Lett. 336, 284-288, 1993
 A:Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial
 A:Reference number: S40463; MUID:94085623; PMID:8262247
 A:Accession: S40463
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-228 <PUN>
 A:Cross-references: UNIPROT:P51525; EMBL:X75438; NID:G443812; PIDN:CAA53188.1; PID:G443812
 R:Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V.
 Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
 A:Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte
 A:Reference number: S57330; MUID:96042752; PMID:7576250
 A:Accession: S57331
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-228 <STR>
 R:Zhao, C.; Ganz, T.; Lehrer, R.I.
 PFBs Lett. 376, 130-134, 1995
 A:Title: Structures of genes for two cathelin-associated antimicrobial peptides: proph
 A:Reference number: S68232; MUID:96105365; PMID:7498526
 A:Accession: S68233
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-228 <ZHA>
 A:Cross-references: EMBL:X89202; NID:G1165148; PIDN:CAA61488.1; PID:G1165149

Db 215 RPPFPGRPPR 227

RESULT 7

A33507
 hypothetical protein DUC-1 - human
 C:Species: Homo sapiens (man)
 C>Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 09-Jul-2004
 C:Accession: A33507
 R:Fujii, H.; Shimada, T.
 J. Biol. Chem. 264, 10057-10064, 1989
 A:Title: Isolation and characterization of cDNA clones derived from the divergently tran
 A:Reference number: A33507; MUID:89255490; PMID:2722860
 A:Accession: A33507
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1137 <FUJ>
 A:Cross-references: UNIPROT:P205085; GB:J04810; NID:G181841; PIDN:AAB47281.1; PID:G181842

Query Match 58.9%; Score 56.5; DB 2; Length 1137;
 Best Local Similarity 62.5%; Pred. No. 21;
 Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 2 RPPFPGRPPR 16

Db 64 PAPPAPPPOLPHV 79

RESULT 8

I51691
 dishevelled homolog - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: I51691
 R:Sokol, S.Y.; Klingensmith, J.; Perrimon, N.; Itoh, K.
 Development 121, 1637-1647, 1995
 A:Title: Dorsalizing and neuralizing properties of Xdsh, a maternally expressed Xenopus
 A:Reference number: I51691; MUID:95324391; PMID:7600981
 A:Accession: I51691
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-736 <SOK>
 A:Cross-references: UNIPROT:P51142; EMBL:U31552; NID:G945109; PIDN:AAB00688.1; PID:G94511

Query Match 58.3%; Score 56; DB 2; Length 736;
 Best Local Similarity 64.3%; Pred. No. 16;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPPPPPPRLPP 14

Db 98 RPPPPPPVPPPP 111

RESULT 9

T30351
 mucin-like protein - Lymantria dispar nuclear polyhedrosis virus
 C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T30351
 R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohrn
 Virology 253, 17-34, 1999
 A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di
 A:Reference number: Z20836; MUID:99124785; PMID:9887315
 A:Accession: T30351
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1029 <KUZ>
 A:Cross-references: UNIPROT:O9YMX0; EMBL:AF081810; PIDN:AACT0189.1

Query Match 57.8%; Score 55.5; DB 2; Length 1029;
 Best Local Similarity 52.4%; Pred. No. 25;
 Matches 11; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 1 RPR-----PPPPPPRLPP 14

Db 927 RPRYSQQPQPQPQPQPQPQP 947

RESULT 10

T26608
 hypothetical protein Y37A1B.2a - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T26608
 R:McMurray, A.
 submitted to the EMBL Data Library, June 1998
 A:Reference number: Z20245
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-164 <WIL>
 A:Cross-references: UNIPROT:O9XXG3; EMBL:AL023835; PIDN:CAA19486.1; GSPDB:GN00022; CESP:Y

Query Match 58.9%; Score 56.5; DB 2; Length 1137;
 Best Local Similarity 62.5%; Pred. No. 21;
 Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 2 RPPFPGRPPR 16

A:Gene: CESP.Y37A1B.2a
A:Map position: 4 66/3
A:Introns: 32/3; 66/3

Query Match 57.3%; Score 55; DB 2; Length 164;
Best Local Similarity 75.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 RPPFFPPRLPP 14
||||| |||||
DB 63 RPPVLPPLPP 74

RESULT 11

C69432
hypothetical protein AF1460 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: C69432
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: C69432
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-227 <KLE>
A:Cross-references: UNIPROT:Q28812; GB:AE001002; GB:AE000782; NID:g2689325; PIDN:AAB8979

Query Match 57.3%; Score 55; DB 2; Length 227;
Best Local Similarity 72.7%; Pred. No. 6.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RPPFFPPRLPP 14
||||| |||||
DB 2 RPPMTPPKLPP 12

RESULT 12

T26998
hypothetical protein Y48B6A.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26998
R:Wall, M.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z20297
A:Accession: T26998
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-716 <WIL>
A:Cross-references: UNIPROT:Q9U2A6; EMBL:AL110490; NID:e1542263; PIDN:CAB54442.1; CESP:Y
A:Experimental source: clone Y48B6A
C:Genetics:
A:Gene: CESP.Y48B6A.6
A:Introns: 38/3; 196/3; 437/2; 460/3; 518/1; 617/3; 673/3

Query Match 57.3%; Score 55; DB 2; Length 716;
Best Local Similarity 69.2%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RPPFFPPRLPP 14
||||| |||||
DB 197 RPPPTSPPLPP 209

RESULT 13

A55624
fibrillin-1 precursor - mouse

C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A55624
R:Yin, W.; Smiley, E.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez, I.
J. Biol. Chem. 270, 1798-1806, 1995
A:Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin ger
A:Reference number: A55624; MUID:95130561; PMID:7829516
A:Accession: A55624
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2871 <YIN>
A:Cross-references: UNIPROT:Q61554; GB:L29454; NID:g575509; PIDN:AAA56840.1; PID:g575510
C:Genetics:
A:Gene: Fbn-1
A:Superfamily: fibrillin; EGF homology
F:1201-1236/Domain: EGF homology <EGF>

Query Match 57.3%; Score 55; DB 2; Length 2871;
Best Local Similarity 58.8%; Pred. No. 81;
Matches 10; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 2 PRPPP--FFPRLPPRI 16
||||| :|||:
DB 428 PRPPEVLYPSREPPRV 444

RESULT 14

T84490
embryo-specific protein 3 (ATS3) - Arabidopsis thaliana
N:Alternate names: protein T28J14.i30
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T84490
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Len
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24493
A:Accession: T84490
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-213 <BEV>
A:Cross-references: UNIPROT:Q9LYP6; EMBL:AL163652
A:Experimental source: cultivar Columbia; BAC clone T28J14
C:Genetics:
A:Map position: 5
A:Introns: 28/3; 65/3
A:Note: T28J14.i30

Query Match 56.2%; Score 54; DB 2; Length 213;
Best Local Similarity 72.7%; Pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPPFFPPRLPP 14
||||| |||||
DB 160 PPHFPPEPPFP 170

RESULT 15

TPCHTC
troponin T, cardiac muscle, embryonic splice form - chicken
N:Contains: cardiac muscle troponin T, adult splice form
C:Species: Gallus gallus (chicken)
C:Date: 28-Aug-1985 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: A25373; A03086
R:Cooper, T.A.; Ordahl, C.P.
J. Biol. Chem. 260, 11140-11148, 1985
A:Title: A single cardiac troponin T gene generates embryonic and adult isoforms via deve
A:Reference number: A25373; MUID:85289327; PMID:2993302
A:Accession: A25373
A:Molecule type: mRNA
A:Residues: 1-302 <COO>
A:Cross-references: UNIPROT:P02642; GB:M10013; NID:g212783; PIDN:AAA49099.1; PID:g212784
R:Cooper, T.A.; Ordahl, C.P.
Science 226, 979-982, 1984

A;Title: A single troponin T gene regulated by different programs in cardiac and skeletal muscle
A;Reference number: A03086; MUID:85065747; PMID:6095446

A:Accession: A03086
A:Accession: A03086
A:Molecule type: mRNA
A:Residues: 68-302 <CO2>
A:Cross-references: GB:K02263; NID:Q212781; PID:AAA9098.1; PID:Q212782
C:Comment: This protein, found in adult cardiac muscle and transiently in embryonic skeletal muscle, is involved in the regulation of the protein in the late stages of skeletal muscle development.
C:Superfamily: troponin T
C:Keywords: alternative splicing; cardiac muscle; differentiation; heart; muscle; phosphatase; troponin T; troponin T, cardiac muscle, embryonic splice form #status predicted <NA>
F1:1-22-33-302/Product: troponin T, cardiac muscle, adult splice form #status predicted <NA>

```
Query Match      56.2%; Score 54; DB 1; Length 302;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

Qy 1 RPRPPPPFPRLPPRI 16
:|:|:|:|:|:|
Db 78 KPKPKPFMPNLPVPPKI 93

Search completed: October 26, 2005, 05:19:59
Job time : 12.9273 secs

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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:52:03 ; Search time 55.4182 Seconds
(without alignments)
147.844 Million cell updates/sec

Title: US-10-014-147-5
Perfect score: 96
Sequence: 1 RRRPPPPPPRLPPRI 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	172	1 PR39_PIG	P80054 sus scrofa
2	63	65.6	378	1 FBSH_HUMAN	Q8R089 mus musculus
3	61	63.5	103	2 Q99FW9	Q99FW9 human papill
4	61	63.5	301	2 Q41848	Q41848 zea mays (m
5	61	63.5	2113	2 Q7PG39	Q7PG39 anopheles g
6	60	62.5	328	2 Q96F80	Q96F80 homo sapien
7	60	62.5	378	2 Q8WVN3	Q8WVN3 homo sapien
8	60	62.5	508	2 Q99LH0	Q99LH0 mus musculus
9	60	62.5	513	2 Q8BWK7	Q8BWK7 mus musculus
10	60	62.5	520	2 Q9H077	Q9H077 homo sapien
11	60	62.5	545	2 Q9DBB2	Q9DBB2 mus musculus
12	60	62.5	581	2 Q9DB24	Q9DB24 mus musculus
13	60	62.5	594	2 Q6UN15	Q6UN15 homo sapien
14	59	61.5	347	1 DTX3_HUMAN	Q8N919 homo sapien
15	59	61.5	347	1 DTX3_MOUSE	Q8N919 mus musculus
16	59	61.5	1395	2 Q7SC01	Q7SC01 neurospora
17	59	61.5	2584	2 Q9TW88	Q9TW88 caenorhabdi
18	59	61.5	2606	2 Q21920	Q21920 caenorhabdi
19	58	60.4	105	2 Q6ETT6	Q6ETT6 oryza sativ
20	58	60.4	139	2 Q6H843	Q6H843 oryza sativ
21	58	60.4	150	2 Q6V7V4	Q6V7V4 oryza sativ
22	58	60.4	150	2 Q6Z4P0	Q6Z4P0 oryza sativ
23	58	60.4	212	1 PF11_PIG	P51534 sus scrofa
24	58	60.4	228	1 PF12_PIG	P51525 sus scrofa
25	58	60.4	586	2 Q63ZL7	Q63ZL7 xenopus lae
26	58	60.4	806	2 Q6CQH5	Q6CQH5 kluyveromyc
27	57	59.4	187	2 Q9FG86	Q9FG86 arabidopsis
28	57	59.4	228	2 Q6Z8Z0	Q6Z8Z0 oryza sativ
29	57	59.4	333	2 Q9X1Z3	Q9X1Z3 oryza sativ
30	57	59.4	348	2 Q6ESK7	Q6ESK7 oryza sativ
31	57	59.4	625	2 Q8S9B5	Q8S9B5 volvox cart

32	57	59.4	825	2 Q7S9H3	Q7S9H3 neurospora
33	56.5	58.9	541	2 Q7RYV7	Q7RYV7 neurospora
34	56.5	58.9	1137	1 MSH3_HUMAN	P20585 homo sapien
35	56.5	58.9	1140	2 Q86UQ6	Q86UQ6 homo sapien
36	56	58.3	165	2 Q6ZL86	Q6ZL86 oryza sativ
37	56	58.3	196	2 Q7X1I7	Q7X1I7 oryza sativ
38	56	58.3	372	1 FBSH_HUMAN	Q9HAH7 homo sapien
39	56	58.3	484	2 Q8ILO0	Q8ILO0 plasmodium
40	56	58.3	721	2 Q6NTP8	Q6NTP8 xenopus lae
41	56	58.3	736	1 DVL2_XENLA	P51142 xenopus lae
42	55.5	57.8	1029	2 Q9YMX0	Q9YMX0 lymantria d
43	55	57.3	164	2 Q9XXG3	Q9XXG3 caenorhabdi
44	55	57.3	205	2 Q9FI79	Q9FI79 arabidopsis
45	55	57.3	227	1 YB60_ARCFU	O28812 archaeoglob

ALIGNMENTS

RESULT 1
PR39_PIG
ID PR39_PIG STANDARD; PRT; 172 AA.
AC P80054; Q9TR84;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antibacterial protein PR-39 precursor.
GN Name=PR39;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95350216; PubMed=7624374;
RA Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,
RA Andersson L., Boman H.G.;
RT "Structure of the gene for porcine peptide antibiotic PR-39, a
RT cathelin gene family member; comparative mapping of the locus for the
RT human peptide antibiotic FALL-39.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=94071853; PubMed=8250863;
RA Storici P., Zanetti M.;
RT "A cDNA derived from pig bone marrow cells predicts a sequence
RT identical to the intestinal antibacterial peptide PR-39.";
RL Biochem. Biophys. Res. Commun. 196:1058-1065(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;
RA Zhao C., Ganz T., Lehrer R.I.;
RT "Structures of genes for two cathelin-associated antimicrobial
RT peptides: prophenin-2 and PR-39.";
RL FEBS Lett. 376:130-134(1995).
RN [4]
RP SEQUENCE OF 131-169.
RC TISSUE=Intestine;
RX MEDLINE=92111534; PubMed=1765098;
RA Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
RA Mutt V., Joernvall H.;
RT "Amino acid sequence of PR-39. Isolation from pig intestine of a new
RT member of the family of proline-arginine-rich antibacterial
RT peptides.";
RL Eur. J. Biochem. 202:849-854(1991).
RN [5]
RP SEQUENCE OF 131-164, AND FUNCTION.
RC TISSUE=Neutrophils;
RX MEDLINE=95088504; PubMed=7996056;
RA Shi J., Ross C.R., Chengappa M.M., Blecha F.;
RT "Identification of a proline-arginine-rich antibacterial peptide from

neutrophils that is analogous to PR-39, an antibacterial peptide from the small intestine.";

-!- FUNCTION: Exerts a potent antimicrobial activity against both E.coli and B.megaterium.

-!- TISSUE SPECIFICITY: Small intestine and bone marrow.

-!- SIMILARITY: Belongs to the cathelicidin family.

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EMBL; X87236; CAA60682.1; -
EMBL; L23825; AAA31109.1; -
EMBL; X89201; CAA61487.1; -
PIR; S68232; S68232.
HSP; F32196; IKWI.
InterPro; IPR001894; Cathelicidin.
Pfam; PF00566; Cathelicidins; 1.
ProDom; PD001838; Cathelicidins; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Amidation; Antibiotic; Direct protein sequencing;
Pyroglutamate carboxylic acid; signal.
SIGNAL 1 29 Potential.
FT PROPEP 30 130
FT CHAIN 131 169
FT MOD_RES 30 30
FT DISULFID 85 96
FT DISULFID 107 124
FT MOD_RES 169 169
FT CONFLICT 21 21 G -> A (in Ref. 2).
FT CONFLICT 29 29 A -> T (in Ref. 1).
FT CONFLICT 90 91 RQ -> QR (in Ref. 1).
FT CONFLICT 117 119 IHS -> NDP (in Ref. 1).
FT CONFLICT 157 157 P -> I (in Ref. 5).
FT SEQUENCE 172 AA; 19476 MW; 994B792798C0E133 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPPPRLPPRI 16
DB 141 RPRPPPPPPRLPPRI 156
|||||

RESULT 2
FESH_MOUSE
ID FESH_MOUSE STANDARD; PRT; 378 AA.
AC Q8R089;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable fibrosin 1 long transcript protein.
GN Name=Fbs1; Synonyms=Fbs;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kani A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maitais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- CAUTION: This CDS has been thought to correspond to fibrosin 1,
but the fibrosin 1 sequence which has been characterized (AC
Q60791) is found in the 3'UTR of these cDNAs. They could
correspond to alternatively spliced isoforms.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

EMBL; AK037952; -; NOT ANNOTATED_CDS.
DR EMBL; BC027193; AAH27193.1; -
DR MGD; MGI:104648; Fbs1.
FT DOMAIN 223 246 Ala-rich.
FT DOMAIN 260 273 Pro-rich.
FT CONFLICT 195 195 A -> T (in Ref. 1).
SQ SEQUENCE 378 AA; 39456 MW; 4C3FAP0D4AC29E69 CRC64;

Query Match 65.6%; Score 63; DB 1; Length 378;
Best Local Similarity 73.3%; Pred. No. 11;

Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPPPPPPRLPPR 15
| | | | |
DB 259 RRRPPPPFLGSLPER 273

RESULT 3

Q99FW9 PRELIMINARY; PRT; 103 AA.
AC Q99FW9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Putative E4 protein.
OS Human papillomavirus type 84.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=150546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21066735; PubMed=11145894; DOI=10.1006/viro.2000.0716;
RA Terai M., Burk R.D.;
RT "Complete nucleotide sequence and analysis of a novel human
RT papillomavirus (HPV 84) genome cloned by an overlapping PCR method.";
RL Virology 279:109-115(2001).
DR EMBL; AF293960; AAK09275.1; -;
DR InterPro; IPR003861; Papilloma_E4.
DR Pfam; PF02711; Pap_E4; 1.
SQ SEQUENCE 103 AA; 11162 MW; 2C32F1FD23337E55 CRC64;

Query Match 63.5%; Score 61; DB 2; Length 103;
Best Local Similarity 73.3%; Pred. No. 5.1;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPPPPPPRLPPR 15
| | | | |
DB 31 RRRPPPSAAPRLPPR 45

RESULT 4

Q41848 PRELIMINARY; PRT; 301 AA.
AC Q41848;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prolin rich protein.
GN Name=PRP; (Maize).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=W64A;
RX MEDLINE=92361259; PubMed=1498600;
RA Jose-Estanyol M., Ruiz-Avila L., Puigdomenech P.;
RT "A maize embryo-specific gene encodes a proline-rich and hydrophobic
RT protein.";
RL Plant Cell 4:413-423(1992).
DR EMBL; X60432; CAA42959.1; -;
DR PIR; JQ1663; JQ1663.
DR HSSP; P24337; IHYP.
DR InterPro; IPR003612; AAI.
DR Pfam; PF00234; Trp_alpha_aml; 1.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 301 AA; 31647 MW; 884EB70854D28C2E CRC64;

Query Match 63.5%; Score 61; DB 2; Length 301;
Best Local Similarity 64.3%; Pred. No. 15;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPPPPPPRLPP 14
| | | | |
DB 179 RPSPPPYVPYVPP 192

RESULT 5

Q7POG9 PRELIMINARY; PRT; 2133 AA.
AC Q7POG9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000020211 (Fragment).
GN Name=ENSANG0000001772;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB801008888; EAA08848.2; -;
DR HSSP; P01130; ID2J.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow fac_recept.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002172; LDL_receptor_A.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00052; Laminin_B; 3.
DR Pfam; PF00053; Laminin_EGF; 4.
DR Pfam; PF00057; Ldl_recept_a; 5.
DR PRINTS; P00261; LDLRECEPTOR.
DR ProDom; PD003031; Laminin_B; 3.
DR PROSITE; PS00022; EGF 1; 7.
DR PROSITE; PS01186; EGF 2; 4.
DR PROSITE; PS50835; IG LIKE; 9.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 7.
DR PROSITE; PS01209; LDLRA_1; 5.
DR PROSITE; PS50068; LDLRA_2; 5.
KW Laminin EGF-like domain.
FT NON_TER 1
FT NON_TER 2133 2133
SQ SEQUENCE 2133 AA; 235646 MW; 16E7ADC733959F6C CRC64;

Query Match 63.5%; Score 61; DB 2; Length 2133;
Best Local Similarity 75.0%; Pred. No. 16+02;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RRRPPPPRLPP 14
| | | | |
DB 1941 RPSYPPRLPP 1952

RESULT 6

Q96F80 PRELIMINARY; PRT; 328 AA.
AC Q96F80;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to RIKEN cDNA 1300019H17 gene (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC011543; AAH11543.1; -.
FT NON_TER
SQ SEQUENCE 328 AA; 37615 MW; 38472A76B3E8A1B9 CRC64;

  Query Match      62.5%; Score 60; DB 2; Length 328;
  Best Local Similarity 75.0%; Pred. No. 21;
  Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPPPPFPPLRP 14
Db 89 KPPPPFPFGAPP 100

RESULT 7
Q8WVN3 PRELIMINARY; PRT; 378 AA.
AC Q8WVN3;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE FIP1L1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC003263; AAH03263.1; -.
DR MGD; MGI:1914149; Fip1l1.
DR InterPro; IPR007854; Fip1.
DR Pfam; PF05182; Fip1; 1.
SQ SEQUENCE 508 AA; 55796 MW; 01BF436596282ED4 CRC64;

  Query Match      62.5%; Score 60; DB 2; Length 508;
  Best Local Similarity 75.0%; Pred. No. 32;
  Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPPPPFPPLRP 14
Db 354 KPPPPFPFGAPP 365

RESULT 9
Q8WVX7 PRELIMINARY; PRT; 513 AA.
AC Q8WVX7;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
enriched library, clone: C530020P17 product: weakly similar to TOMATO
CELL WALL HRGP (HYDROXYPROLINE-RICH GLYCOPROTEIN) (Fragment).
DE NCBI_TaxID=10090;
GN Name=Fip1l1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC003263; AAH03263.1; -.
DR MGD; MGI:1914149; Fip1l1.
DR InterPro; IPR007854; Fip1.
DR Pfam; PF05182; Fip1; 1.
SQ SEQUENCE 508 AA; 55796 MW; 01BF436596282ED4 CRC64;

  Query Match      62.5%; Score 60; DB 2; Length 508;
  Best Local Similarity 75.0%; Pred. No. 32;
  Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPPPPFPPLRP 14
Db 354 KPPPPFPFGAPP 365
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RN Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RN Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RN Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK049672; BAC33867.1; -
DR MGD; MGI:1914149; F01p11.
DR InterPro; IPR007854; F01p1.
DR Pfam; PF05182; F01p1.
FT NON TER 513 513
SQ SEQUENCE 513 AA; 57835 MW; CC9CD61F7A0C2062 CRC64;

Query Match 62.5%; Score 60; DB 2; Length 513;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPPPPPPPPRLPP 14
DB 295 KPPPPPPPPGAPP 306

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RESULT 10
Q9H077 PRELIMINARY; PRT; 520 AA.
ID Q9H077
AC Q9H077;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein DKFZp586K0717.
GN Name=DKFZp586K0717;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RG The German cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; ALI36910; CAB6844.1; -
DR Genew; HGNC:19124; F01p1.
DR InterPro; IPR007854; F01p1.
DR Pfam; PF05182; F01p1.
KW Hypothetical protein.
SQ SEQUENCE 520 AA; 58375 MW; 55D48285A046A783 CRC64;

Query Match 62.5%; Score 60; DB 2; Length 520;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPPPPPPPPRLPP 14
DB 281 KPPPPPPPPGAPP 292

RESULT 11
Q9DBB2 PRELIMINARY; PRT; 545 AA.
ID Q9DBB2
AC Q9DBB2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male liver cDNA, RIKEN full-length enriched
DE library, clone:1300019H17 product:weakly similar to TOMATO CELL WALL
DE HRGP (HYDROXYPROLINE-RICH GLYCOPROTEIN).
GN Name=F01p1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RN Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
the RIKEN Genome Exploration Research Group Phase I & II Team;
RN [3]

```

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RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Hayashizaki Y., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX STRAIN=C57BL/6J; Arai A., Aono H.,
RA Adachi J., Aizawa K., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Kouda M., Kasukawa T., Kato H.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK005061; BAB23785.1; -
DR MGD; MGI:1914149; Fip1l1.
DR InterPro; IPR007854; Fip1.
DR Pfam; PF05182; Fip1; 1.
SQ SEQUENCE 545 AA; 61059 MW; D8C65A7E20CA0985 CRC64;
Query Match 62.5%; Score 60; DB 2; Length 545;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 RPPPPPPRLPP 14
Db 295 KPPPPPPGAPP 306
:|||||
:|||||
:|||||

RESULT 12
Q9D824 PRELIMINARY; PRT; 581 AA.
AC Q9D824;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus adult male small intestine cDNA, RIKEN full-length
DE enriched library, clone:2010310H23 product:weakly similar to TOMATO
DE CELL WALL HRGP (HYDROXYPROLINE-RICH GLYCOPROTEIN).
GN Name=Fip1l1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX STRAIN=C57BL/6J; Arai A., Aono H.,
RA Adachi J., Aizawa K., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Kouda M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK005061; BAB23785.1; -
DR MGD; MGI:1914149; Fip1l1.
DR InterPro; IPR007854; Fip1.
DR Pfam; PF05182; Fip1; 1.
SQ SEQUENCE 545 AA; 61059 MW; D8C65A7E20CA0985 CRC64;
Query Match 62.5%; Score 60; DB 2; Length 581;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 RPPPPPPRLPP 14
Db 331 KPPPPPPGAPP 342
:|||||
:|||||
:|||||

RESULT 13

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Q6UN15 PRELIMINARY; PRT; 594 AA.
 AC Q6UN15;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Pre-mRNA 3' end processing factor FIP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RN
 RC TISSUE=Testis;
 RC PubMed=14749727; DOI=10.1038/sj.emboj.7600070;
 RX Kaufmann I., Martin G., Friedlein A., Langen H., Keller W.;
 RT "Human Fip1 is a subunit of CPFG that binds to U-rich RNA elements and
 RT stimulates poly(A) polymerase.";
 RL EMBO J. 23:616-626(2004).
 DR EMBL; AY366510; AAQ89277.1; --
 DR InterPro; IPR007854; Fip1.
 DR Pfam; PF05182; Fip1; 1.
 DR
 SQ SEQUENCE 594 AA; 66526 MW; B391D142419ED061 CRC64;
 Query Match: 62.5%; Score 60; DB 2; Length 594;
 Best Local Similarity 75.0%; Pred. No. 38;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 RPPPPPPPPRLPP 14
 DB 355 KPFPFPFGAPP 366
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 DTX3 HUMAN STANDARD; PRT; 347 AA.
 ID DTX3 HUMAN Q8N919; Q8N919; Q8N919;
 AC Q8N919; Q8N919; Q8N919;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Deltex protein 3 (Deltex-3) (Deltex3).
 GN Name=DTX3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Cerebellum, and Teratocarcinoma;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara T., Sano S.,
 RA Mariya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe K., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,

RA Mateumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN
 RP SEQUENCE OF 4-201 FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RC Bloecker H., Boecher M., Brandt P., Mewes H.-W., Weil B., Wiemann S.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP IN VITRO UBIQUITIN LIGASE ACTIVITY.
 RX MEDLINE=22679154; PubMed=12670957; DOI=10.1074/jbc.M301157200;
 RA Takeyama K., Aguilar R.C.T., Gu L., He C., Freeman G.J., Kutok J.L.,
 RA Aster J.C., Shipp M.A.;
 RT "The BAL-binding protein isopeptidase and related Deltex family members
 RT exhibit ubiquitin-protein isopeptidase activity.";
 RL J. Biol. Chem. 278:21930-21937(2003).
 CC -!- FUNCTION: Regulator of Notch signaling, a signaling pathway
 CC involved in cell-cell communications that regulates a broad
 CC spectrum of cell-fate determinations. Probably acts both as a
 CC positive and negative regulator of Notch, depending on the
 CC developmental and cell context (By similarity). Functions as an
 CC ubiquitin ligase protein in vitro, suggesting that it may regulate
 CC the Notch pathway via some ubiquitin ligase activity.
 CC -!- SUBUNIT: Homomultimer. May form a heteromultimer with other
 CC members of the Deltex family. Interacts with NOTCH1 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8N919-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8N919-2; Sequence=VSP 008354;
 CC Note=No experimental confirmation available;
 CC -!- SIMILARITY: Belongs to the Deltex family.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AK092085; BAC03801.1; --
 CC EMBL; AK094385; BAC04344.1; --
 CC EMBL; AL831941; CAD38593.1; --
 CC Genew; HGNC:24457; DTX3.
 CC InterPro; IPR001841; Znf_ring.
 CC Pfam; PF00097; zf-C3HC4; 1.
 CC SMART; SM00184; RING; 1.
 CC PROSITE; PS00518; ZF_RING_1; 1.
 CC PROSITE; PS50089; ZF_RING_2; 1.
 CC Alternative splicing; Metal-binding; Notch signaling pathway; Zinc;
 CC Zinc-finger.
 FT ZN FING 164 205 RING-type.
 FT DOMAIN 122 151 Pro-rich.
 FT VARSPPLIC 1 7 MSFVLSR->MPILSSGSK (in isoform 2).
 FT
 SQ SEQUENCE 347 AA; 37988 MW; FDB4CDC982F1B707 CRC64;
 Query Match: 61.5%; Score 59; DB 1; Length 347;
 Best Local Similarity 66.7%; Pred. No. 29;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 RPPPPPPPPRLPPRI 16
 | | | | | | | | | |

Db 139 PPPPPPLPPLPRL 153

RESULT 15
DTX3 MOUSE
AC DTX3 MOUSE STANDARD; PRT; 347 AA.
ID Q80V1. Q9ER06;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Deltex protein 3 (Deltex-3) (Deltex3) (mDTX3).
GN Name=Dtx3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxId=10090;
RX [1]
RN SEQUENCE FROM N.A., TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND
RP MULTIMERIZATION
RX MEDLINE=21123790; PubMed=11226752; DOI=10.1016/S0736-5748(00)00071-X;
RA Kishi N., Tang Z., Maeda Y., Hirai A., Mo R., Ito M., Suzuki S.,
RA Nakao K., Kinoshita T., Kadesch T., Hui C.-C., Artavanis-Tsakonas S.,
RA Okano H., Matsuno K.;
RA "Murine homologs of dltex define a novel gene family involved in
RT vertebrate Notch signaling and neurogenesis.";
RT Int'. J. Dev. Neurosci. 19:21-35 (2001).
RN [2]
RN SEQUENCE FROM N.A.
RP RP
RC TISUUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Regulator of Notch signaling, a signaling pathway
involved in cell-cell communications that regulates a broad
spectrum of cell-fate determinations. Probably acts both as a
positive and negative regulator of Notch, depending on the
developmental and cell context. Functions as an ubiquitin ligase
protein in vitro, suggesting that it may regulate the Notch
pathway via some ubiquitin ligase activity (By similarity).
CC -!- SUBUNIT: Homomultimer. May form a heteromultimer with other
members of the Deltex family. Interacts with NOTCH1.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- TISSUE SPECIFICITY: Strongly expressed in testis and brain. Weakly
expressed in kidney.
CC -!- DEVELOPMENTAL STAGE: In the CNS, it is expressed in the developing
neural tube starting from E10.5 in the spinal cord and around
E11.5 in the telencephalon. Expressed ubiquitously throughout the
spinal cord and telencephalon during neurogenesis. Expressed
throughout the developing retina at E15.5. Not expressed in the
somite or presumote during somitogenesis. Expressed slightly later
than Dtx2.
CC -!- SIMILARITY: Belongs to the Deltex family.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to a chimeric
cDNA.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:02:04 ; Search time 16.4364 Seconds
(without alignments)
72.667 Million cell updates/sec

Title: US-10-014-147-5

Perfect score: 96

Sequence: 1 RRRPPPPPPRLPPRI 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/6C COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	96	100.0	16	3	US-09-024-975-3
2	96	100.0	16	4	US-08-930-777A-5
3	96	100.0	23	4	US-08-930-777A-3
4	96	100.0	26	2	US-08-419-066-2
5	96	100.0	26	3	US-09-024-975-2
6	96	100.0	26	4	US-08-930-777A-2
7	96	100.0	38	4	US-09-739-535-1
8	96	100.0	39	1	US-08-162-052-1
9	96	100.0	39	1	US-08-310-722-1
10	96	100.0	39	2	US-08-419-066-1
11	96	100.0	39	2	US-08-728-333-1
12	96	100.0	39	3	US-09-024-975-1
13	96	100.0	39	4	US-08-930-777A-1
14	96	100.0	39	5	PCT-US95-12080-1
15	63	65.6	31	3	US-09-179-558-66
16	63	65.6	31	4	US-09-722-825-66
17	63	65.6	31	4	US-09-722-487-66
18	63	65.6	31	4	US-09-722-708-66
19	60	62.5	52	1	US-09-149-476-392
20	59	61.5	31	3	US-08-957-351-9
21	57	59.4	15	4	US-08-930-777A-6
22	57	59.4	19	4	US-08-930-777A-4
23	56.5	58.9	1137	4	US-09-538-092-968
24	55	57.3	78	1	US-08-487-359-5
25	55	57.3	78	1	US-08-487-359-7
26	55	57.3	78	1	US-08-222-798A-5
27	55	57.3	78	1	US-08-222-798A-7

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29	55	57.3	79	1	US-08-487-359-2	Sequence 2, Appli
30	55	57.3	79	1	US-08-487-359-3	Sequence 3, Appli
31	55	57.3	79	1	US-08-487-359-8	Sequence 8, Appli
32	55	57.3	79	1	US-08-222-798A-1	Sequence 1, Appli
33	55	57.3	79	1	US-08-222-798A-2	Sequence 2, Appli
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35	55	57.3	79	1	US-08-222-798A-8	Sequence 8, Appli
36	55	57.3	107	4	US-09-253-991A-32013	Sequence 32013, A
37	55	57.3	442	4	US-09-248-796A-21400	Sequence 21400, A
38	54	56.2	511	4	US-09-107-433-2904	Sequence 2904, Ap
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41	52	54.2	79	1	US-08-487-359-4	Sequence 4, Appli
42	52	54.2	79	1	US-08-222-798A-4	Sequence 4, Appli
43	52	54.2	97	4	US-09-489-039A-10835	Sequence 10835, A
44	52	54.2	433	4	US-09-949-016-6497	Sequence 6497, Ap
45	52	54.2	802	4	US-09-823-240A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-024-975-3
; Sequence 3, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-024-975-3

Query Match 100.0%; Score 96; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2,1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPPPPRLPPRI 16
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Db      1 RRRPPPPPPRLPPRI 16

RESULT 2
US-08-930-777A-5
; Sequence 5, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-930-777A-3

Query Match      100.0%; Score 96; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPPPPPPRLPPRI 16
        |||||
DB      8 RRRPPPPPPRLPPRI 23

RESULT 4
US-08-419-066-2
; Sequence 2, Application US/08419066
; Patent No. 5810993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; MOLECULE TYPE: peptide
; US-08-930-777A-5

Query Match      100.0%; Score 96; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPPPPPPRLPPRI 16
        |||||
DB      1 RRRPPPPPPRLPPRI 16

RESULT 3
US-08-930-777A-3
; Sequence 3, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:

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Db      1 RRRPPPPPPRLPPRI 16

RESULT 2
US-08-930-777A-5
; Sequence 5, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-930-777A-3

Query Match      100.0%; Score 96; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPPPPPPRLPPRI 16
        |||||
Db      8 RRRPPPPPPRLPPRI 23

RESULT 4
US-08-419-066-2
; Sequence 2, Application US/08419066
; Patent No. 5810993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; MOLECULE TYPE: peptide
; US-08-930-777A-5

Query Match      100.0%; Score 96; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPPPPPPRLPPRI 16
        |||||
Db      1 RRRPPPPPPRLPPRI 16

RESULT 3
US-08-930-777A-3
; Sequence 3, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:

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Db      1 RRRPPPPPPRLPPRI 16

RESULT 2
US-08-930-777A-5
; Sequence 5, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-930-777A-3

Query Match      100.0%; Score 96; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPPPPPPRLPPRI 16
        |||||
Db      8 RRRPPPPPPRLPPRI 23

RESULT 4
US-08-419-066-2
; Sequence 2, Application US/08419066
; Patent No. 5810993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; MOLECULE TYPE: peptide
; US-08-930-777A-5

Query Match      100.0%; Score 96; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPPPPPPRLPPRI 16
        |||||
Db      1 RRRPPPPPPRLPPRI 16

RESULT 3
US-08-930-777A-3
; Sequence 3, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-2

Query Match 100.0%; Score 96; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPPPFPRLPPRI 16
Db 11 RRRPPPPFPRLPPRI 26

RESULT 5
US-09-024-975-2
; Sequence 2, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-024-975-2

Query Match 100.0%; Score 96; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPPPFPRLPPRI 16
Db 11 RRRPPPPFPRLPPRI 26

RESULT 6
US-08-930-777A-2
; Sequence 2, Application US/08930777A
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; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-930-777A-2

Query Match 100.0%; Score 96; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPPPFPRLPPRI 16
Db 11 RRRPPPPFPRLPPRI 26

RESULT 7
US-09-739-535-1
; Sequence 1, Application US/09739535
; Patent No. 6794490
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/739,535
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-739-535-1

Query Match 100.0%; Score 96; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RRRPPPPPPRLPPRI 16
Db 11 RRRPPPPPPRLPPRI 26

RESULT 8
US-08-162-052-1
; Sequence 1, Application US/08162052
; Patent No. 5489575
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong-Youn
; APPLICANT: BOWAN, Hans G
; APPLICANT: MUTTI, Viktor
; APPLICANT: JORNWALL, Hans
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,052
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: SE 9101838-2
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92-22578
; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 003300-299
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-162-052-1

Query Match 100.0%; Score 96; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPPPPRLPPRI 16
Db 11 RRRPPPPPPRLPPRI 26

RESULT 9
US-08-310-722-1
; Sequence 1, Application US/08310722
; Patent No. 5654273
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,722
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: CMCC379
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Boman, Hans G.
; AUTHORS: Mutt, Viktor
; AUTHORS: Jornvall, Hans
; TITLE: No. 5654273el Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-310-722-1

Query Match 100.0%; Score 96; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPPPPRLPPRI 16
Db 11 RRRPPPPPPRLPPRI 26

RESULT 10
US-08-419-066-1
; Sequence 1, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Boman, Hans G.
; AUTHORS: Mutt, Viktor
; AUTHORS: Jorvall, Hans
; TITLE: No. 5863897el Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
;
US-08-728-333-1
Query Match 100.0%; Score 96; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRPDPFPFPLPPRI 16
| | | | | | | | | | | | | | | |
Db 11 RRPDPFPFPLPPRI 26

RESULT 12
US-09-024-975-1
; Sequence 1, Application US/09024975
; Patent No. 613233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-09-024-975-1
Query Match 100.0%; Score 96; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRPDPFPFPLPPRI 16
| | | | | | | | | | | | | | | |
Db 11 RRPDPFPFPLPPRI 26

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RESULT 13
US-08-930-777A-1
; Sequence 1, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-930-777A-1

Query Match 100.0%; Score 96; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPPPPRLPPRI 16
DB 11 RRRPPPPPPRLPPRI 26

RESULT 14
PCT-US95-12080-1
; Sequence 1, Application PC/TUS9512080
; GENERAL INFORMATION:
; APPLICANT: Children's Medical Center Corporaton
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12080
; FILING DATE:
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-815-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Roman, Hans G.
; AUTHORS: Mutt, Viktor
; AUTHORS: Jornvall, Hans
; TITLE: Novel Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
PCT-US95-12080-1

Query Match 100.0%; Score 96; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPPPPRLPPRI 16
DB 11 RRRPPPPPPRLPPRI 26

RESULT 15
US-09-179-558-66
; Sequence 66, Application US/09179558
; Patent No. 6180612
; GENERAL INFORMATION:
; APPLICANT: Hockensmith, Joel W.
; APPLICANT: Muthuswami, Rohini
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TARGETING DNA METABOLIC PROCESSES USING
; TITLE OF INVENTION: AMINOGLYCOSIDE DERIVATIVES
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/179,558
; FILING DATE: 27-OCT-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 09/060,470
; FILING DATE: 15-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 60/063,898
; FILING DATE: 31-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742

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REFERENCE/DOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-179-558-66

Query Match 65.6%; Score 63; DB 3; Length 311;
Best Local Similarity 70.6%; Pred. No. 2.1;
Matches 12; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 2 PRPPPF---PRRLPP 14
DB 26 PRPPPFPSLPPRLPP 42

Search completed: October 26, 2005, 05:21:58
Job time : 17.4364 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:05:05 ; Search time 59.0545 Seconds
(without alignments)
113.119 Million cell updates/sec

Title: US-10-014-147-5

Perfect score: 96

Sequence: 1 RRRPPPPPPRLPPRI 16

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Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	96	100.0	16	15	US-10-651-147-5
3	96	100.0	23	14	US-10-014-147-3
4	96	100.0	23	15	US-10-651-147-3
5	96	100.0	26	14	US-10-014-147-2
6	96	100.0	26	15	US-10-651-147-2
7	96	100.0	38	9	US-09-738-742-1
8	96	100.0	38	9	US-09-739-535-1
9	96	100.0	39	14	US-10-014-147-1
10	96	100.0	39	15	US-10-391-155-1
11	96	100.0	39	15	US-10-391-155-2

12	96	100.0	39	15	US-10-391-155-6
13	96	100.0	39	15	US-10-651-147-1
14	96	100.0	42	15	US-10-344-709C-18
15	96	100.0	42	17	US-10-916-185-14
16	96	100.0	42	18	US-10-931-286A-44
17	96	100.0	42	20	US-11-004-379-20
18	75	78.1	304	14	US-10-156-761-13550
19	66	68.8	91	16	US-10-425-115-200180
20	65	67.7	153	16	US-10-425-115-208716
21	63	65.6	129	16	US-10-425-115-224656
22	63	65.6	232	16	US-10-425-115-190616
23	62	64.6	90	16	US-10-437-963-126573
24	62	64.6	182	16	US-10-425-115-346674
25	62	64.6	187	16	US-10-425-115-220493
26	62	64.6	333	16	US-10-437-963-169542
27	61	63.5	132	16	US-10-767-701-51171
28	61	63.5	209	16	US-10-425-115-207591
29	61	63.5	256	16	US-10-437-963-128526
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31	61	63.5	322	16	US-10-425-115-316075
32	60	62.5	191	16	US-10-425-115-285148
33	60	62.5	204	16	US-10-437-963-180133
34	60	62.5	425	16	US-10-437-963-108858
35	60	62.5	431	16	US-10-437-963-204963
36	60	62.5	520	9	US-09-726-643-102
37	60	62.5	520	13	US-10-042-141-102
38	60	62.5	520	17	US-10-919-272-102
39	60	62.5	521	10	US-09-809-391-392
40	60	62.5	521	10	US-09-882-171-392
41	60	62.5	521	15	US-10-164-861-392
42	60	62.5	526	9	US-09-925-300-1473
43	59.5	62.0	80	15	US-10-424-599-231660
44	59	61.5	103	15	US-10-424-599-258982
45	59	61.5	204	16	US-10-425-115-342021

ALIGNMENTS

RESULT 1

US-10-014-147-5
; Sequence 5, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-014-147-5
Query Match 100.0%; Score 96; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPRPPPPPPRLPPRI 16
Db 1 RPRPPPPPPRLPPRI 16
RESULT 2
US-10-651-147-5
; Sequence 5, Application US/10651147
; Publication No. US20040043934A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/651,147
; FILING DATE: 28-Aug-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-651-147-5
Query Match 100.0%; Score 96; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPRPPPPPPRLPPRI 16

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Db 1 RPRPPPPPPRLPPRI 16
RESULT 3
US-10-014-147-3
; Sequence 3, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-014-147-3
Query Match 100.0%; Score 96; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPRPPPPPPRLPPRI 16
Db 8 RPRPPPPPPRLPPRI 23
RESULT 4
US-10-651-147-3
; Sequence 3, Application US/10651147
; Publication No. US20040043934A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.

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ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/651,147
FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-651-147-3
Query Match 100.0%; Score 96; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPPPPPPRLPPRI 16
Db 8 RRRPPPPPPRLPPRI 23
RESULT 5
US-10-014-147-2
Sequence 2, Application US/10014147
Publication No. US20030125249A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-014-147-2
Query Match 100.0%; Score 96; DB 14; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 11 RRRPPPPPPRLPPRI 26
RESULT 6
US-10-651-147-2
Sequence 2, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/651,147
FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-651-147-2
Query Match 100.0%; Score 96; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPPPPPPRLPPRI 16

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Db      11 RRRPPPPPPRLPPRI 26
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US-09-738-742-1
; Sequence 1, Application US/09738742
; Publication No. US20020025924A1
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/738,742
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-738-742-1
Query Match      100.0%; Score 96; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPPPPPPRLPPRI 16
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Db      11 RRRPPPPPPRLPPRI 26
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US-09-739-535-1
; Sequence 1, Application US/09739535
; Publication No. US20020058785A1
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/739,535
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-739-535-1
Query Match      100.0%; Score 96; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPPPPPPRLPPRI 16
|||||
Db      11 RRRPPPPPPRLPPRI 26
|||||
US-10-014-147-1
; Sequence 1, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; Shi, Jishu
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; ATTORNEY/AGENT INFORMATION:
; CLASSIFICATION: Unknown
; FILING DATE: 18-Mar-2003
; APPLICATION NUMBER: US/10/391,155
; CURRENT APPLICATION DATA:
; SOFTWARE: WordPerfect version 10
; OPERATING SYSTEM: MS XP
; COMPUTER: Dell PC
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; ZIP: 01930
; COUNTRY: USA
; STATE: Massachusetts
; CITY: Magnolia
; STREET: P.O. Box 5387
; ADDRESSEE: David Prashker, Esq.
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 6
; TITLE OF INVENTION: Method for PR-39 peptide mediated selective inhibition of IkBA degradation
; APPLICANT: Simons, Michael
; Gao, Youhe
; Sequence 1, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated selective inhibition of IkBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: WordPerfect version 10
; APPLICATION NUMBER: US/10/391,155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 23625-A
; REGISTRATION NUMBER: 26,262
; NAME: Collins, John M.
; FILING DATE: April 10, 1996
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: US/08/930,777A
; CLASSIFICATION: 530
; FILING DATE: 07-Dec-2001
; APPLICATION NUMBER: US/10/014,147
; CURRENT APPLICATION DATA:
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; OPERATING SYSTEM: PC-DOS/MS-DOS
; COMPUTER: IBM PC compatible
; MEDIUM TYPE: Floppy disk
; ZIP: 64108
; COUNTRY: U.S.A.
; STATE: Missouri
; CITY: Kansas City
; STREET: 2405 Grand Blvd., Ste. 400
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-014-147-1
Query Match      100.0%; Score 96; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPPPPPPRLPPRI 16
|||||
Db      11 RRRPPPPPPRLPPRI 26
|||||
RESULT 10
US-10-391-155-1
; Sequence 1, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated selective inhibition of IkBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: WordPerfect version 10
; APPLICATION NUMBER: US/10/391,155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 23625-A
; REGISTRATION NUMBER: 26,262
; NAME: Collins, John M.
; FILING DATE: April 10, 1996
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: US/08/930,777A
; CLASSIFICATION: 530
; FILING DATE: 07-Dec-2001
; APPLICATION NUMBER: US/10/014,147
; CURRENT APPLICATION DATA:
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; OPERATING SYSTEM: PC-DOS/MS-DOS
; COMPUTER: IBM PC compatible
; MEDIUM TYPE: Floppy disk
; ZIP: 64108
; COUNTRY: U.S.A.
; STATE: Missouri
; CITY: Kansas City
; STREET: 2405 Grand Blvd., Ste. 400
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-014-147-1
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; REFERENCE/DOCKET NUMBER: BIS-044/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-391-155-1
Query Match 100.0%; Score 96; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPPPPPRLPPRI 16
Db 11 RRRPPPPPPRLPPRI 26

RESULT 11
US-10-391-155-2
; Sequence 2, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated
; selective inhibition of IKBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: WordPerfect version 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-044/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-391-155-6
Query Match 100.0%; Score 96; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPPPPPRLPPRI 16
Db 11 RRRPPPPPPRLPPRI 26

RESULT 12
US-10-391-155-6
; Sequence 6, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated
; selective inhibition of IKBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: WordPerfect version 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-044/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-391-155-6
Query Match 100.0%; Score 96; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPPPPPRLPPRI 16
Db 11 RRRPPPPPPRLPPRI 26

RESULT 13
US-10-651-147-1
; Sequence 1, Application US/10651147
; Publication No. US20040043934A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/10/651,147
; FILING DATE: 28-Aug-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-651-147-1
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Query Match 100.0%; Score 96; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RRPFPFPFPPRLPPRI 16
| | | | | | | | | | | | | | | |
Db 11 RRPFPFPFPPRLPPRI 26
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RESULT 14

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US-10-344-709C-18
; Sequence 18, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
; APPLICANT: JORG FRITZ ET AL.
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof
; FILE REFERENCE: SONN:030US
; CURRENT APPLICATION NUMBER: US/10/344,709C
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: A 1416/2000
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-18
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Query Match 100.0%; Score 96; DB 16; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RRPFPFPFPPRLPPRI 16
| | | | | | | | | | | | | | | |
Db 11 RRPFPFPFPPRLPPRI 26
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RESULT 15

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US-10-916-185-14
; Sequence 14, Application US/10916185
; Publication No. US20050107325A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
```

```
; APPLICANT: Kesavan, Venkatasamy
; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: MODIFIED iRNA AGENTS
; FILE REFERENCE: 14174-091001
; CURRENT APPLICATION NUMBER: US/10/916,185
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US2004/011829
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/506,341
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 60/510,246
; PRIOR FILING DATE: 2003-10-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptides
US-10-916-185-14
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Query Match 100.0%; Score 96; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RRPFPFPFPPRLPPRI 16
| | | | | | | | | | | | | | | |
Db 11 RRPFPFPFPPRLPPRI 26
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Search completed: October 26, 2005, 05:28:57
Job time : 60.0545 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 04:51:43 ; Search time 59.0455 Seconds
(without alignments)
98.253 Million cell updates/sec

Title: US-10-014-147-6

Perfect score: 92
Sequence: 1 RIPPQFPFRPPRP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003a:*
- 7: Geneseq2003b:*
- 8: Geneseq2004s:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	15	AAW01449	Leukocyte
2	92	100.0	15	ADE86117	Proline-a
3	92	100.0	15	ADL67259	Antimicro
4	92	100.0	39	AAR30491	Antibacte
5	92	100.0	39	AAR99121	Magalinin-
6	92	100.0	39	AAR94446	Synducin
7	92	100.0	39	AAW01446	Leukocyte
8	92	100.0	39	AAW57222	Proline/a
9	92	100.0	39	AAB26888	PR-39 pep
10	92	100.0	39	AAB37280	PR-39 pep
11	92	100.0	39	AAB84690	Amino aci
12	92	100.0	39	ADD35364	Antimicro
13	92	100.0	39	ADE86112	Proline-a
14	92	100.0	39	ADL67254	Antimicro
15	92	100.0	42	ABB07714	Cell perm
16	92	100.0	42	ADR82250	E. coli A
17	92	100.0	44	AAB51194	Human hea
18	57.5	62.5	366	ADJ69455	Leukocyte
19	57	62.0	16	AAW01448	Proline/a
20	57	62.0	16	AAW5724	Proline-a
21	57	62.0	16	ADE86116	Proline-a
22	57	62.0	16	ADL67258	Antimicro
23	57	62.0	23	AAW01451	Leukocyte
24	57	62.0	23	ADE86114	Proline-a
25	57	62.0	23	ADL67256	Antimicro

ALIGNMENTS

RESULT 1

AAW01449
ID AAW01449 standard; peptide; 15 AA.

XX AC AAW01449;

XX AC AAW01449;

DT 18-JUN-1997 (first entry)

DE Leukocyte O2- production inhibitor peptide PR15.

KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
antimicrobial peptide; small intestine; human; neutrophil; bacteria;
DNA synthesis; protein synthesis; inhibitor; syndecan expression;
mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
tissue damage; oxygen radical; inflammatory disease; therapy.

OS Synthetic.

PN WO9632129-A1.

XX PD 17-OCT-1996.

XX PF 10-APR-1996; 96WO-US004674.

XX PF 10-APR-1995; 95US-00419066.

XX PA (UNIV) UNIV KANSAS STATE RES FOUND.

XX PI Blecha F, Shi J;

XX PS WPI; 1996-476842/47.

XX PT Inhibition of leukocyte superoxide anion prodn. and attraction of
leukocytes - using peptide(s) partic. based on antimicrobial PR-39.

XX CC Claim 12; Page 28; 45pp; English.

CC AAW01447-W01454 represent fragments of the proline-arginine rich
antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
isolated from porcine small intestine, and has also been identified in
human and porcine neutrophils. PR39 kills bacteria by interfering with
DNA and/or protein synthesis. PR39 also induces syndecan expression on
mesenchymal cells. Syndecans are important in wound repair, showing that
PR39 can be used in wound repair, as well as in antibacterial agents.
These sequences, and PR39, can be used in the method of the invention.
The method of the invention is for inhibiting leukocyte superoxide anion
(O2-) production. The method comprises administering to a leukocyte a
peptide (such as this sequence) capable of inhibiting leukocyte O2-

AAW01447 Leukocyte
AAW5724 Proline-a
ADE86113 Proline-a
ADL67255 Antimicro
AAY05824 Arabidops
ADC38726 Human sec
ABO44410 Novel hum
ABO44402 Novel hum
ABO44394 Novel hum
ABO44386 Novel hum
ABO44407 Novel hum
ABO44399 Novel hum
ABO44391 Novel hum
ABO44383 Novel hum
ADN03630 Antipsori
ADL11120 Human the
ABO44409 Novel hum
ABO44401 Novel hum
ABO44393 Novel hum
ABO44385 Novel hum

CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting tissue
 CC damage at the wound site caused by excessive oxygen radicals produced by
 CC these leukocytes. They can also be used to develop products for treating
 CC inflammatory disease states

XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 92; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRPPRP 15
 DB 1 RPPGFPFRPPRP 15

RESULT 2
 ADE86117
 ID ADE86117 standard; peptide; 15 AA.

XX AC ADE86117;

XX DT 29-JAN-2004 (first entry)

XX DE Proline-arginine (PR)-rich antimicrobial peptide PR-15.

XX KW Leukocyte superoxide anion; leukocyte O2- production;
 KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;
 KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;
 KW tissue damage; oxygen radical; antibacterial.

XX OS Synthetic.

XX PN US2003125249-A1.

XX PD 03-JUL-2003.

XX PF 07-DEC-2001; 2001US-00014147.

XX PR 10-APR-1995; 95US-00419066.

XX PR 08-OCT-1997; 97US-00930777.

XX PA (BLEC/) BLECHA F.

XX PA (SHIJ/) SHI J.

XX PI Blecha F, Shi J;

XX DR WPI; 2004-059188/06.

XX PT Attracting leukocyte to location by administering peptide including
 PT proline-arginine-rich antimicrobial peptide or its truncated analogs to
 PT the location.

XX PS Claim 3; SEQ ID NO 6; 24pp; English.

XX CC The present invention relates to a method of inhibiting leukocyte
 CC superoxide anion (O2-) production and/or attracting leukocytes. The
 CC method comprises the use of proline-arginine (PR)-rich antimicrobial
 CC peptides or their truncated analogues. The method is useful for
 CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or
 CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are
 CC useful as medicaments to fight infection by attracting leukocytes to a
 CC wound site, while restricting tissue damage at the wound site caused by
 CC excessive oxygen radicals produced by these leukocytes. The present
 CC sequence represents a PR-rich antimicrobial peptide.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 92; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRPPRP 15
 DB 1 RPPGFPFRPPRP 15

RESULT 3

ADL67259
 ID ADL67259 standard; peptide; 15 AA.

XX AC ADL67259;

XX DT 20-MAY-2004 (first entry)

XX DE Antimicrobial peptide PR-39 analog PR-15.

XX KW Leucocyte; superoxide anion; oxygen radical; proline-arginine;
 KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;
 KW infection; wound; tissue damage; PR-39 analog; PR-15.

XX OS Unidentified.

XX PN US2004043934-A1.

XX PD 04-MAR-2004.

XX PF 28-AUG-2003; 2003US-00651147.

XX PR 10-APR-1995; 95US-00419066.

XX PR 08-OCT-1997; 97US-00930777.

XX PA (BLEC/) BLECHA F.

XX PA (SHIJ/) SHI J.

XX PI Blecha F, Shi J;

XX DR WPI; 2004-225728/21.

XX PT Inhibiting leukocyte oxygen radical production comprises contacting a
 PT leukocyte with a peptide, where the inhibition occurs as a consequence of
 PT binding between the peptide and p47phox.

XX PS Example; SEQ ID NO 6; 24pp; English.

XX CC The invention relates to inhibiting leukocyte superoxide anion (O2-)
 CC production using a naturally occurring proline-arginine (PR)-rich
 CC antimicrobial peptide known as PR-39 and its truncated analogs. The
 CC method comprises contacting leukocytes with the peptide comprising 39 or
 CC 26 amino acids, for a time and under conditions effective to inhibit
 CC leukocyte superoxide anion production. The peptide inhibits the activity
 CC of NADPH oxidase responsible for anion production, by binding to Src
 CC homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein
 CC of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or
 CC porcine leukocyte and the mammalian leukocyte is neutrophil. Another
 CC method is also disclosed which employs a PR-39 analog that comprise 16
 CC amino acids, where the sum of the proline and arginine residues in the
 CC effective peptide is at least 66 or 74 % of the total number of amino
 CC acids. This peptide inhibits leukocyte O2- production by the effective
 CC binding to p47phox in whole cells, therefore interfering with the binding
 CC of p47phox to p22phox. At least 14 or 25% of the amino acid residues in
 CC the peptide are arginine residues. The method of the invention is useful
 CC for inhibiting leukocyte oxygen radical production. The peptides are
 CC useful as medicaments for fighting infections by attracting leukocytes to
 CC a wound site, yet restrict tissue damage at the wound site caused by
 CC excessive oxygen radicals produced by these leukocytes. The present
 CC sequence is PR-39 analog, PR-15.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 92; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRPPRP 15

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Db      1 RPPGPPPPPPRFP 15
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RESULT 4
AAR30491
ID AAR30491 standard; peptide; 39 AA.
XX
AC AAR30491;
XX
XX 25-MAR-2003 (revised)
DT 12-MAY-1993 (first entry)
XX
XX Antibacterial peptide.
DE
XX Pig; small intestine; endocrine; gram negative; bacteria; therapeutic;
KW veterinary medicine; prophylactic.
KW
XX Sus scrofa domestica.
OS
XX WO9222578-A1.
PN
XX 23-DEC-1992.
PD
XX 10-JUN-1992; 92WO-SF000394.
PF
XX 14-JUN-1991; 91SE-00001838.
PR
XX (LEEJ/) LEE J.
PA (BOMA/) BOMAN H. G.
PA (MUTT/) MUTT V.
PA (JOER/) JOERNVALL H.
XX
XX Lee J, Boman HG, Mutt V, Joernvall H;
PI WPI; 1993-018080/02.
XX
XX New anti-bacterial polypeptide - active against Gram negative bacteria.
PT
XX Claim 1; Page 10; 15pp; English.
PS
XX This peptide was isolated from the small intestine of a pig. The small
CC intestine is an important endocrine organ and many physiologically active
CC peptides have been isolated from it. This peptide inhibits the growth of,
CC and may kill, bacteria. pref. gram negative bacteria. This peptide or its
CC functional derivatives may be used in human or veterinary medicine for
CC therapeutic or prophylactic use. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 39 AA;
SQ
      Query Match      100.0%; Score 92; DB 2; Length 39;
      Best Local Similarity 100.0%; Pred. No. 0.00044;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RPPGPPPPPPRFP 15
      |||||
Db      25 RPPGPPPPPPRFP 39
      |||||
RESULT 5
AAR99121
ID AAR99121 standard; peptide; 39 AA.
XX
AC AAR99121;
XX
XX 28-OCT-1996 (first entry)
DT
XX Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.
DE
XX STD; sexually transmitted disease; HIV; human immunodeficiency virus;
KW herpes simplex virus; HSV; Neisseria gonorrhoeae; Candida; Chlamydia;
KW magainin; antimicrobial; squalamine.

```

```

XX OS Synthetic.
XX FH Key
FT Modified-site 39 Location/Qualifiers
FT FT 39 /note= "amidated"
XX PN WO9608270-A2.
XX XX
XX PD 21-MAR-1996.
XX
XX PF 13-SEP-1995; 95WO-US011675.
XX
XX PR 13-SEP-1994; 94US-00305475.
XX
XX PA (MAGA-) MAGAININ PHARM INC.
XX
XX PI Jacob L, Zasloff M, Williams T, Bedi G;
XX WPI; 1996-179725/18.
XX
XX Inhibiting sexually transmitted disease e.g. HIV or herpes simplex - by
PT administering magainin antimicrobial or squalamine cpd. to inhibit
PT transmission.
XX
XX Example 1; Page 32; 60pp; English.
PS
XX AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may be
CC used to treat sexually transmitted diseases (STDs) caused by Chlamydia,
CC HIV, herpes simplex virus, Neisseria gonorrhoeae or Candida infection.
CC The peptides inhibit STDs by either killing the infectious organism,
CC impeding the infection mechanism or interrupting the replication cycle of
CC the organism. Squalamine (an aminoesterol host defence molecule of the dog
CC fish shark Squalus acanthias) and PGLa (a frog antimicrobial peptide)
CC analogues may also be useful in inhibiting STD infection and transmission
XX
XX Sequence 39 AA;
SQ
      Query Match      100.0%; Score 92; DB 2; Length 39;
      Best Local Similarity 100.0%; Pred. No. 0.00044;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RPPGPPPPPPRFP 15
      |||||
Db      25 RPPGPPPPPPRFP 39
      |||||
RESULT 6
AAR94446
ID AAR94446 standard; peptide; 39 AA.
XX
AC AAR94446;
XX
XX 05-NOV-1996 (first entry)
DT
XX Synducin peptide (PR-39) induces syndecan expression.
DE
XX Synducin; induction; expression; syndecan-1; syndecan-4; surface;
KW mesenchymal cell; fibroblast; epithelial; PR-39; treatment; stasis;
KW decubitus; ulcers; keloids; skin burns; ischemic tissues;
KW hypercoagulation states; prevention; tumour metastasis; restenosis;
KW inhibition; angiogenesis; proliferation; endothelial.
XX
XX Synthetic.
XX OS
XX WO9609322-A2.
PN
XX 28-MAR-1996.
PD
XX 22-SEP-1995; 95WO-US012080.
PF
XX 22-SEP-1994; 94US-00310722.
PR
XX
XX

```

PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX Gallo RL, Bernfield M;
 PI WPI; 1996-188401/19.
 XX Modulating mesenchymal interaction by administration of synducin - used
 PT in the treatment of wounds, tumors, restenosis, etc.
 XX Claim 4; Page 26; 34pp; English.
 PS The present peptide is a synducin, which induces the expression of
 CC syndecan-1 and syndecan-4 on the surface of mesenchymal cells, esp.
 CC fibroblasts and epithelial cells. The 36 N-terminal amino acids of the
 CC peptide were found to be identical to the 36 N-terminal amino acids of PR
 CC -39, a Pro and Arg rich antibacterial peptide previously found in porcine
 CC intestine (WO9222578). Synducins may be used in the treatment of stasis
 CC and decubitus ulcers, keloids, skin burns, ischemic tissues and
 CC hypercoagulation states; prevention of tumor metastasis, restenosis
 CC inhibition and endothelial cell angiogenesis and proliferation induction.
 CC Human microvascular endothelial cells were assayed for syndecan-4
 CC expression following exposure to 5 % wound fluid, dbcAMP (1 mM), the
 CC present peptide (10 microm) or a blank, to give respective cell surface
 CC syndecan-4 values (mod/m in) of approx. 1.75, 1.70, 1.80 and 0.95
 XX
 SQ Sequence 39 AA;

Query Match 100.0%; Score 92; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRPPRP 15
 |||||
 DB 25 RPPGFPFRPPRP 39

RESULT 7
 AAW01446
 ID AAW01446 standard; peptide; 39 AA.
 XX
 AC AAW01446;
 XX
 DT 18-JUN-1997 (first entry)
 XX
 DE Leukocyte O2- production inhibitor peptide PR39.
 XX
 KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
 KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 KW tissue damage; oxygen radical; inflammatory disease; therapy.
 XX
 OS Synthetic.
 XX
 PN WO9632129-A1.
 XX
 PD 17-OCT-1996.
 XX
 PF 10-APR-1996; 96WO-US004674.
 XX
 PR 10-APR-1995; 95US-00419066.
 XX
 PA (UNIV) UNIV KANSAS STATE RES FOUND.
 XX
 PI Blecha F, Shi J;
 XX
 DR WPI; 1996-476842/47.
 XX
 PT Inhibition of leukocyte super:oxide anion prodn. and attraction of
 PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.
 XX
 PS Claim 2; Page 26; 45pp; English.
 XX

CC This sequence represents the proline-arginine rich antimicrobial peptide
 CC PR39. The PR39 sequence was first isolated from porcine small intestine,
 CC and has also been identified in human and porcine neutrophils. PR39 kills
 CC bacteria by interfering with DNA and/or protein synthesis. PR39 also
 CC induces syndecan expression on mesenchymal cells. Syndecans are important
 CC in wound repair, showing that PR39 can be used in wound repair, as well
 CC as in antibacterial agents. This sequence, and the fragments of it shown
 CC in AAW01447-W01454, can be used in the method of the invention. The
 CC method of the invention is for inhibiting leukocyte superoxide anion (O2-
 CC) production. The method comprises administering to a leukocyte a peptide
 CC (such as this sequence) capable of inhibiting leukocyte O2- production.
 CC The peptides can be used as medicaments for fighting infection by
 CC attracting leukocytes to a wound site and restricting tissue damage at
 CC the wound site caused by excessive oxygen radicals produced by these
 CC leukocytes. They can also be used to develop products for treating
 CC inflammatory disease states
 SQ Sequence 39 AA;

Query Match 100.0%; Score 92; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRPPRP 15
 |||||
 DB 25 RPPGFPFRPPRP 39

RESULT 8
 AAW75722
 ID AAW75722 standard; peptide; 39 AA.
 XX

AC AAW75722;

XX 19-NOV-1998 (first entry)

XX Proline/Arginine rich peptide PR-39.

XX Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;
 KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;
 KW coronary bypass; organ transplantation surgery.

XX Synthetic.

XX WO9835690-A1.

XX 20-AUG-1998.

XX 17-FEB-1998; 98WO-US003207.

XX 18-FEB-1997; 97US-00802306.

PR 16-FEB-1998; 98US-00024975.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Ross CR, Blecha F, Shi J;

XX WPI; 1998-495359/42.

XX Reduction of reperfusion injury in temporarily occluded blood vessels -
 PT by administration of a peptide which is rich in proline or arginine
 PT residues.

XX Claim 3; Page 14; 35pp; English.

XX Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
 CC administration into a mammal's bloodstream reduce reperfusion injury
 CC (production of reactive oxygen species, neutrophil adherence to
 CC endothelium, and extravasation of neutrophils). These peptides have two
 CC requirements: they contain the consensus sequence PXXP, where P is a
 CC proline residue and X is any amino acid residue, which has been found to
 CC inhibit superoxide production, and secondly they have arginine residues
 CC adjacent to these motifs, required for effective inhibition. It was

QY 1 RPPGPPRRPPRRPP 15
 |||||
 Db 25 RPPGPPRRPPRRPP 39

RESULT 11

AAB84690
 ID AAB84690 standard; protein; 39 AA.

XX AC AAB84690;

XX DT 17-SEP-2001 (first entry)

XX DE Amino acid sequence of a PR-39 protein.

XX PR-39; IkappaBalpha degradation; NfkappaB transcription factor;
 KW myocardial infarction; chronic myocardial ischemia; heart disease;
 KW anoxia.

XX OS Unidentified.

XX PN WO200147540-A1.

XX PD 05-JUL-2001.

XX PF 27-DEC-2000; 2000WO-US035293.

XX PR 29-DEC-1999; 99US-00474967.

XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX PI Simons M, Gao Y;

XX DR WPI; 2001-441690/47.

XX PT Selective inhibition of IkappaBalpha degradation within targeted viable
 PT cell collection, involves interacting PR-39 oligopeptide with
 PT IkappaBalpha and proteasomes, and altering proteolytic activity of
 PT proteasomes.

XX PS Disclosure; Page 30; 69pp; English.

XX CC The present sequence represents a PR-39 protein. The specification
 CC describes PR-39 derived peptides, which are used for selective inhibition
 CC of IkappaBalpha degradation within a targeted cell collection in-situ.
 CC The method is useful for selectively inhibiting IkappaBalpha protein
 CC degradation in situ, decreasing the activity of NfkappaB transcription
 CC factor and selective control of NfkappaB-dependent gene expression in
 CC situ. The PR-39 derived peptides are useful in the treatment of
 CC myocardial infarction, chronic myocardial ischemia of heart disease and
 CC anoxia

XX SQ Sequence 39 AA;

Query Match 100.0%; Score 92; DB 4; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGPPRRPPRRPP 15
 |||||
 Db 25 RPPGPPRRPPRRPP 39

RESULT 12

ADD35364
 ID ADD35364 standard; peptide; 39 AA.

XX AC ADD35364;

XX DT 15-JAN-2004 (first entry)

XX DE Antimicrobial peptide PR-39.

XX antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological;
 KW intraocular pressure; glaucoma; ocular hypertension; hyperaemia;
 KW irritation; inflammation; conjunctiva; ocular cell dysplasia;
 KW iridial melanocyte hyperplasia; hyperpigmentation.

XX OS Unidentified.

XX PN WO2003079997-A2.

XX PD 02-OCT-2003.

XX PF 21-MAR-2003; 2003WO-US008935.

XX PR 21-MAR-2002; 2002US-0367071P.

XX PA (CAYM-) CAYMAN CHEM CO.

XX PI Maxey KM, Johnson J;

XX DR WPI; 2004-011506/01.

XX PT Ophthalmic solution useful for the treatment of increased intraocular
 PT pressure comprises a prostaglandin of the F-series and an antimicrobial
 PT peptide.

XX PS Disclosure; Page 11; 11pp; English.

XX CC The invention relates to a novel ophthalmic solution comprising a
 CC prostaglandin of the F-series and an antimicrobial peptide. A solution of
 CC the invention has hypotensive and ophthalmological activity. The solution
 CC is useful for the treatment of increased intraocular pressure, such as
 CC caused by glaucoma and for the reduction of ocular hypertension. The
 CC prostaglandin and the antimicrobial peptide work synergistically, to
 CC provide beneficial reduction in the incidence of irritant and toxic side
 CC effects such as hyperaemia, irritation and inflammation of conjunctiva,
 CC ocular cell dysplasia, iridial melanocyte hyperplasia, and
 CC hyperpigmentation, associated with the prior art prostaglandin
 CC compositions. The present sequence represents an antimicrobial peptide of
 CC the invention.

XX SQ Sequence 39 AA;

Query Match 100.0%; Score 92; DB 8; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGPPRRPPRRPP 15
 |||||
 Db 25 RPPGPPRRPPRRPP 39

RESULT 13

ADE86112
 ID ADE86112 standard; peptide; 39 AA.

XX AC ADE86112;

XX DT 29-JAN-2004 (first entry)

XX DE Proline-arginine (PR)-rich antimicrobial peptide PR-39.

XX KW Leukocyte superoxide anion; leukocyte O2- production;
 KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;
 KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;
 KW tissue damage; oxygen radical; antibacterial.

XX OS Synthetic.

XX PN US2003125249-A1.

XX PD 03-JUL-2003.

PF 07-DEC-2001; 2001US-00014147.
XX 10-APR-1995; 95US-00419066.
PR 08-OCT-1997; 97US-00930777.
XX (BLEC/) BLECHA F.
PA (SHIJ/) SHI J.
XX Blecha F, Shi J;
XX WPI; 2004-059188/06.
XX Attracting leukocyte to location by administering peptide including
PT proline-arginine-rich antimicrobial peptide or its truncated analogs to
FT the location.
XX Claim 2; SEQ ID NO 1; 24pp; English.
XX The present invention relates to a method of inhibiting leukocyte
CC superoxide anion (O2-) production and/or attracting leukocytes. The
CC method comprises the use of proline-arginine (PR)-rich antimicrobial
CC peptides or their truncated analogues. The method is useful for
CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or
CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are
CC useful as medicaments to fight infection by attracting leukocytes to a
CC wound site, while restricting tissue damage at the wound site caused by
CC excessive oxygen radicals produced by these leukocytes. The present
CC sequence represents a PR-rich antimicrobial peptide.
XX Sequence 39 AA;
SQ
Query Match 100.0%; Score 92; DB 8; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPPGPPPPPPPP 15
Db 25 RPPGPPPPPPPP 39
RESULT 14
ADL67254
ID ADL67254 standard; peptide; 39 AA.
XX ADL67254;
XX 20-MAY-2004 (first entry)
XX Antimicrobial peptide PR-39.
XX Leucocyte ; superoxide anion; oxygen radical; proline-arginine ;
KW antimicrobial; antioxidant; NADPH oxidase ; p47phox; neutrophil;
KW infection; wound ; tissue damage ; PR-39 peptide.
XX Unidentified.
XX Key Location/Qualifiers
FH Peptide 1. .26
FT /label= PR-26_peptide
FT Peptide 1. .19
FT /label= PR-19_peptide
FT Peptide 1. .14
FT /label= PR-14_peptide
FT Region 1. .3
FT /note= "Essential for antibacterial activity"
FT Peptide 4. .26
FT /label= PR-23_peptide
FT Peptide 11. .26
FT /label= PR-16_peptide
FT Region 20. .26
FT /note= "Essential for antibacterial activity"
FT Peptide 25. .39
FT /label= PR-15_peptide

XX US2004043934-A1.
XX 04-MAR-2004.
XX 28-AUG-2003; 2003US-00651147.
XX 10-APR-1995; 95US-00419066.
PR 08-OCT-1997; 97US-00930777.
XX (BLEC/) BLECHA F.
PA (SHIJ/) SHI J.
XX Blecha F, Shi J;
XX WPI; 2004-225728/21.
XX Inhibiting leukocyte oxygen radical production comprises contacting a
PT leukocyte with a peptide, where the inhibition occurs as a consequence of
PT binding between the peptide and p47phox.
XX Claim 1; SEQ ID NO 1; 24pp; English.
XX The invention relates to inhibiting leukocyte superoxide anion (O2-) production using a naturally occurring proline-arginine (PR)-rich antimicrobial peptide known as PR-39 and its truncated analogs. The method comprises contacting leukocytes with the peptide comprising 39 or 26 amino acids, for a time and under conditions effective to inhibit leukocyte superoxide anion production. The peptide inhibits the activity of NADPH oxidase responsible for anion production, by binding to Src homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or porcine leukocyte and the mammalian leukocyte is neutrophil. Another method is also disclosed which employs a PR-39 analog that comprise 16 amino acids, where the sum of the proline and arginine residues in the effective peptide is at least 66 or 74 % of the total number of amino acids. This peptide inhibits leukocyte O2- production by the effective binding to p47phox in whole cells, therefore interfering with the binding of p47phox to p22phox. At least 14 or 25% of the amino acid residues in the peptide are arginine residues. The method of the invention is useful for inhibiting leukocyte oxygen radical production. The peptides are useful as medicaments for fighting infections by attracting leukocytes to a wound site, yet restrict tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. The present sequence is PR-39 peptide.
XX Sequence 39 AA;
SQ
Query Match 100.0%; Score 92; DB 8; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPPGPPPPPPPP 15
Db 25 RPPGPPPPPPPP 39
RESULT 15
ABB07714
ID ABB07714 standard; peptide; 42 AA.
XX ABB07714;
XX 10-JUN-2002 (first entry)
XX Antimicrobial peptide PR-39 C-terminal fragment.
XX Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response;
KW antigen presenting cell; adjuvant; porcine; PR-39.
XX Sus sp.
XX WO200213857-A2.
PN

XX 21-FEB-2002.
PD
XX
XX
PF 17-AUG-2001; 2001WO-EP009529.
XX
XX
PR 17-AUG-2000; 2000AT-00001416.
XX
XX
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI Fritz J, Mattner F, Zauner W, Buschle M, Egyed A;
XX
XX WPI; 2002-269154/31.
DR
XX
XX Vaccine for active immunization or for preparing an adjuvant for
PT enhancing an immune response to at least one antigen, comprises at least
PT one antigen and at least one cathelicidin derived antimicrobial peptide.
XX
XX
PS Disclosure; Fig 3; 65pp; English.
XX
XX The invention relates to a vaccine comprising at least one antigen and at
CC least one cathelicidin derived antimicrobial peptide or its derivative.
CC The vaccine is useful for active immunization, especially of humans or
CC animals without protection against the specific antigen. The cathelicidin
CC derived antimicrobial peptide is useful in the preparation of an adjuvant
CC for enhancing the immune response to at least one antigen, where the
CC adjuvant enhances the uptake of at least one antigen in antigen
CC presenting cells (APC), and the adjuvant is added to the vaccine.
CC Sequences ABB07708-15 represent C-terminal fragments of antimicrobial
CC peptides of the cathelicidin family
XX
SQ Sequence 42 AA;

Query Match 100.0%; Score 92; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIPPGPPPPPPPPPP 15
|||
Db 25 RIPPGPPPPPPPPPP 39
|||

Search completed: October 26, 2005, 05:12:08
Job time : 60.0455 secs

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:00:14 ; Search time 11.1818 Seconds
(without alignments)
129.071 Million cell updates/sec

Title: US-10-014-147-6

Perfect score: 92

Sequence: 1 RPPGPPPPPPRFP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	92	100.0	172	2 S68232	antimicrobial prot
2	57	62.0	213	2 T48490	embryo-specific pr
3	55	59.8	866	1 JC4305	dynamain II - human
4	54	58.7	428	2 T48008	hypothetical prote
5	53.5	58.2	212	2 S57330	cathelin-like anti
6	53.5	58.2	228	2 S40463	prophenin (PR-2) p
7	53	57.6	741	2 T00206	epidermis-specific
8	53	57.6	1029	2 T30351	mucin-like protein
9	52.5	57.1	1560	2 T42727	proliferation pote
10	52	56.5	134	2 D84672	hypothetical prote
11	52	56.5	388	2 JC5437	spliceosome-associ
12	51.5	56.0	948	2 A57640	retinoblastoma bin
13	51	55.4	743	1 S23779	collagen alpha 1(V
14	51	55.4	744	1 A34246	collagen alpha 1(V
15	51	55.4	744	1 S23298	collagen alpha 1(V
16	51	55.4	744	2 S15435	collagen alpha 1(V
17	51	55.4	868	2 A36878	dynamain 2 - rat
18	51	55.4	870	2 B53165	dynamain II isoform
19	51	55.4	870	2 A53165	dynamain II isoform
20	51	55.4	879	2 D96804	unknown protein T5
21	50	54.3	513	2 T37180	probable membrane
22	49	53.3	424	2 A54964	spliceosome-associ
23	48.5	52.7	147	2 A29149	proline-rich prote
24	48.5	52.7	164	2 A30496	proline-rich prote
25	48.5	52.7	172	2 B29149	proline-rich prote
26	48.5	52.7	204	2 A39066	proline-rich prote
27	48.5	52.7	223	2 A42817	proline-rich prote
28	48.5	52.7	564	2 H70804	hypothetical prote
29	48	52.2	199	2 S14981	extensin class I (

hypothetical prote
Mm-1 cell derived
hypothetical prote
chloride channel p
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
probable U4/U6 sma
Ca2+/calmodulin-de
hypothetical prote
period clock prote
hypothetical prote
hypothetical prote
maternal effect pr

ALIGNMENTS

RESULT 1

S68232
antimicrobial protein PR-39 precursor, cathelin-associated - pig
N/Alternate names: myeloid antibacterial protein PR-39

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S68232; JN0899; I47138; S19563

R/Zhao, C.; Ganz, T.; Lehrer, R.I.

FEBS Lett. 376, 130-134, 1995

A>Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni

A/Reference number: S68232; MUID:96105365; PMID:7498526

A/Accession: S68232

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-172 <SHA>

A/Cross-references: UNIPROT:P80054; EMBL:X89201; NID:g1165150; PIDN:CAA61487.1; PID:g1161

A/Experimental source: leukocytes

R/Storici, P.; Zanetti, M.

Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993

A>Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the i

A/Reference number: JN0899; MUID:94071853; PMID:8250863

A/Accession: JN0899

A/Molecule type: mRNA

A/Residues: 1-20, 'A', 22-172 <STO>

A/Cross-references: GB:I23825; NID:G435100; PIDN:AAA31109.1; PID:G435101

A/Experimental source: bone marrow cells

R/Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bone

Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995

A>Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fami

A/Reference number: I47138; MUID:95350216; PMID:7624374

A/Accession: I47138

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-28, 'T', 30-89, 'QR', 92-116, 'NDP', 120-172 <GUD>

A/Cross-references: EMBL:X67236; NID:G829142; PIDN:CAA60682.1; PID:g1051298

R/Aggerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall,

Eur. J. Biochem. 202, 849-854, 1991

A>Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of th

A/Reference number: S19563; MUID:92111534; PMID:1765098

A/Accession: S19563

A/Molecule type: protein

A/Residues: 131-169 <AGE>

A/Experimental source: intestine

C/Genetics:

A/Gene: PR39

A/Introns: 66/3; 102/3; 126/3

C/Superfamily: cathelin; cystatin homology

C/Keywords: amidated carboxyl end; antibacterial

F;1-29/Domain: signal sequence #status predicted <SIG>

F;22-129/Domain: signal sequence #status predicted <SIG>

F;30-130/Domain: propeptide #status predicted <PRO>

F;131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>

Query Match	59.8%;	Score 55;	DB 1;	Length 866;
Best Local Similarity	66.7%;	Pred. No. 9.7;		

RESULT 6

S40463
 prophenin (PF-2) precursor - pig
 N:Alternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S40463; S57331; S68233
 R:Pungertar, J.; Struelens, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, F.; Turk, F.B.S. Lett. 336, 284-288, 1993
 A:Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial
 A:Reference number: S40463; MUID:94085623; PMID:8262247
 A:Accession: S40463
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-228 <PUN>
 A:Cross-references: UNIPROT:P51525; EMBL:X75438; NID:G443812; PIDN:CAA53188.1; PID:G443812
 R:Struelens, B.; Pungertar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Bexbic, S.; Turk, V. Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
 A:Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte
 A:Reference number: S57330; MUID:96042752; PMID:7576250
 A:Accession: S57331
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-228 <STR>
 R:Zhao, C.; Ganz, T.; Lehrer, R.I. F.B.S. Lett. 376, 130-134, 1995
 A:Title: Structures of genes for two cathelin-associated antimicrobial peptides: proph
 A:Reference number: S68232; MUID:96105365; PMID:7498526
 A:Accession: S68233
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-228 <ZHA>
 A:Cross-references: EMBL:X89202; NID:g1165148; PIDN:CAA61488.1; PID:g1165149
 C:Genetics:
 A:Introns: 66/3; 102/3; 126/3
 C:Superfamily: cathelin; cystatin homology
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:22-129/Domain: cystatin homology <CYS>
 F:30-228/Product: prophenin (PF-2) #status predicted <MAT>
 Query Match 58.2%; Score 53.5; DB 2; Length 228;
 Best Local Similarity 60.0%; Pred. No. 3.8;
 Matches 12; Conservative 0; Mismatches 1; Indels 7; Gaps 2;
 QY 3 PPGFP-PRFP-----PRFP 15
 DB 170 PPNFGPGRPPPPPPPPGPRFP 189
 RESULT 7
 T00206
 C:Species: Ciona savignyi
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T00206
 R:Chiba, S.; Satoh, Y.; Nishikata, T.; Satoh, N.
 A:Description: Isolation and characterization of cDNA clones for tissue-specific genes i
 A:Reference number: Z14123
 A:Accession: T00206
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-741 <CHI>
 A:Cross-references: UNIPROT:O15999; EMBL:AB008818; PIDN:BA023597.1
 C:Superfamily: Ciona savignyi epidermis-specific protein 1; trefol homology
 F:568-610/Domain: trefol homology <TRF>
 Query Match 57.6%; Score 53; DB 2; Length 741;
 Best Local Similarity 72.7%; Pred. No. 15;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 IPGFPFRPP 12
 DB 726 IPPGPPNTPP 736

RESULT 8

T30351
 mucin-like protein - Lymantria dispar nuclear polyhedrosis virus
 C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T30351
 R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohm
 A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di
 A:Reference number: Z20836; MUID:99124785; PMID:9887315
 A:Accession: T30351
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1029 <KUZ>
 A:Cross-references: UNIPROT:Q9YMK0; EMBL:AF081810; PIDN:AACT0189.1

Query Match 57.6%; Score 53; DB 2; Length 1029;
 Best Local Similarity 80.0%; Pred. No. 21;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPGFPFRPP 12
 DB 938 PPGFPFRPP 947

RESULT 9

T42727
 proliferation potential-related protein - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42727
 R:Witte, M.M.; Scott, R.E.
 A:Reference number: Z22246
 A:Accession: T42727
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1560 <WIT>
 A:Cross-references: UNIPROT:P97868; EMBL:U03913; NID:G3858884; PID:G3858885; PIDN:AACT42727
 A:Experimental source: strain Balb/C
 C:Genetics:
 A:Gene: P2P-R
 C:Function:
 A:Description: involved in hMRNP association and Rb1 binding
 F:57-107/Domain: RING finger homology <RRN>

Query Match 57.1%; Score 52.5; DB 2; Length 1560;
 Best Local Similarity 60.0%; Pred. No. 37;
 Matches 9; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 IPPGFPFRPPFRPP 15
 DB 376 LPPGVLPQFSPQFP 390

RESULT 10

DB4672
 hypothetical protein At2g27390 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: DB4672
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umavam, L.; Tallon, L.
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: DB4672
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-134 <STO>

A:Cross-references: UNIPROT:Q9XIP3; GB:AE002093; NID:G5306259; PIDN:AA4191.1; GSPDB:GN
 C:Genetics:
 A:Gene: At2g27390
 A:Map position: 2

Query Match 56.5%; Score 52; DB 2; Length 134;
 Best Local Similarity 60.0%; Pred. No. 3.5;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RPPGFPFRPPRFP 15
 :||| |||
 Db 54 RLPPPPFPALFPPEP 68

RESULT 11
 JC5437
 spliceosome-associated protein 49 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 17-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 16-Aug-2004
 C:Accession: JC5437
 R:Tanaka, Y.; Ohta, A.; Terashima, K.; Sakamoto, H.
 J. Biochem. 121, 739-745, 1997
 A:Title: Polycistronic expression and RNA-binding specificity of the C. elegans homolog
 A:Reference number: JC5437; MUID:97306058; PMID:9163526
 A:Accession: JC5437
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-388 <TAN>
 A:Cross-references: UNIPROT:Q17352; GB:U24189
 C:Comment: This protein is a subunit of splicing factor SF3b and is involved in U2 small
 C:Superfamily: ribonucleoprotein repeat homology
 F:14-97,101-184/Region: RNA recognition pattern
 F:14-81/Domain: ribonucleoprotein repeat homology <RRM4>
 F:101-169/Domain: ribonucleoprotein repeat homology <RRM2>
 F:260-388/Region: proline-rich

Query Match 56.5%; Score 52; DB 2; Length 388;
 Best Local Similarity 60.0%; Pred. No. 10;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RPPGFPFRPPRFP 15
 :||| |||
 Db 342 RYPGMPPPPRYP 356

RESULT 12
 A57640
 retinoblastoma binding protein RBQ-1 - human
 C:Species: Homo sapiens (man)
 C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
 C:Accession: A57640
 R:Sakai, Y.; Saijo, M.; Coelho, T.; Kishino, T.; Niikawa, N.; Taya, Y.
 Genomics 30, 98-101, 1995
 A:Title: cDNA sequence and chromosomal localization of a novel human protein, RBQ-1 (RBE
 A:Reference number: A57640; MUID:96129310; PMID:8595913
 A:Accession: A57640
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-948 <SAK>
 A:Cross-references: UNIPROT:Q15290; GB:X85133; NID:G728590; PIDN:CAA59445.1; PID:G755748
 C:Genetics:
 A:Gene: GDB:RBBP6
 A:Cross-references: GDB:626076
 A:Map position: 16p12-16p11.2
 C:Keywords: tandem repeat; zinc
 F:79-129/Domain: RING finger homology <RNG>

Query Match 56.0%; Score 51.5; DB 2; Length 948;
 Best Local Similarity 60.0%; Pred. No. 30;
 Matches 9; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 IPPGF-PPRPPRFP 15
 :||| |||

Db 398 LPPGVPPQFSPQFP 412

RESULT 13
 S23779
 collagen alpha 1(VIII) chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: S23779
 R:Muragaki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, B.R.; Ninomiya, Y.
 Eur. J. Biochem. 207, 895-902, 1992
 A:Title: Alpha-1(VIII)-collagen gene transcripts encode a short-chain collagen polypeptic
 A:Reference number: S23779; MUID:92362626; PMID:1499564
 A:Accession: S23779
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-743 <MUR>
 A:Cross-references: UNIPROT:Q00780; EMBL:X66976; NID:G50493; PIDN:CAA47387.1; PID:G13599;
 C:Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
 F:616-742/Domain: complement Clq carboxyl-terminal homology <ClQ>

Query Match 55.4%; Score 51; DB 1; Length 743;
 Best Local Similarity 50.0%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPPGFPPRPPRFP 15
 :||| |||
 Db 36 LPPQIPQIPQIP 49

RESULT 14
 A34246
 collagen alpha 1(VIII) chain precursor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A34246
 R:Yamaguchi, N.; Benya, P.D.; van der Rest, M.; Ninomiya, Y.
 J. Biol. Chem. 264, 16022-16029, 1989
 A:Title: The cloning and sequencing of alpha1(VIII) collagen cDNAs demonstrate that type
 omains similar to those of type X collagen.
 A:Reference number: A34246; MUID:89380199; PMID:2476437
 A:Accession: A34246
 A:Molecule type: mRNA
 A:Residues: 1-744 <YAM>
 A:Cross-references: UNIPROT:P14282; GB:J05042; NID:G164895; PIDN:AAA31204.1; PID:G164896
 C:Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
 F:21-117/Region: amino-terminal nonhelical
 F:118-571/Region: interrupted helical
 F:572-744/Region: carboxyl-terminal nonhelical
 F:617-743/Domain: complement Clq carboxyl-terminal homology <ClQ>

Query Match 55.4%; Score 51; DB 1; Length 744;
 Best Local Similarity 50.0%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPPGFPPRPPRFP 15
 :||| |||
 Db 36 LPPQIPQIPQIP 49

RESULT 15
 S23298
 collagen alpha 1(VIII) chain - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: S23298
 R:Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McCa
 maguchi, N.; Olsen, B.R.
 in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pres
 A:Title: The molecular biology of collagens with short triple-helical domains.
 A:Reference number: S22243

A:Accession: S23298
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-744 <NIN>
A:Cross-references: UNIPROT:Q7LZR2
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
P:617-743/Domain: complement C1q carboxyl-terminal homology <CIQ>

Query Match 55.4%; Score 51; DB 1; Length 744;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPPGPPPPPPRPP 15
Db 36 LPPQIPPPQPPQIP 49

Search completed: October 26, 2005, 05:20:01
Job time : 13.1818 secs

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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:52:03 ; Search time 51.9545 Seconds
(without alignments)
147.844 Million cell updates/sec

Title: US-10-014-147-6

Perfect score: 92

Sequence: 1 RPPGFPFRFP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	172	1 PR39 PIG	P80054 sus scrofa
2	67	72.8	484	2 Q81LQ0	Q81LQ0 plasmodium
3	63	68.5	415	2 Q7RQAO	Q7RQAO plasmodium
4	57	62.0	213	2 Q81271	Q81271 arabidopsis
5	57	62.0	213	2 Q94K23	Q94K23 arabidopsis
6	57	62.0	213	2 Q9LVP6	Q9LVP6 arabidopsis
7	56	60.9	135	2 Q61134	Q61134 dictyosteli
8	56	60.9	139	2 Q61135	Q61135 dictyosteli
9	56	60.9	150	2 Q67VV4	Q67VV4 oryza sativ
10	56	60.9	150	2 Q6Z4P0	Q6Z4P0 oryza sativ
11	56	60.9	2382	1 WNK1 HUMAN	Q9H4A3 homo sapien
12	55	59.8	393	2 Q9UPH5	Q9UPH5 homo sapien
13	55	59.8	464	2 Q8N1K8	Q8N1K8 homo sapien
14	55	59.8	870	1 DYN2 HUMAN	P50570 homo sapien
15	54.5	59.2	213	2 Q7SHV3	Q7SHV3 neurospora
16	54	58.7	428	2 Q9MIQ8	Q9MIQ8 arabidopsis
17	54	58.7	480	2 Q740X0	Q740X0 mycobacteri
18	54	58.7	532	2 Q61133	Q61133 dictyosteli
19	54	58.7	851	2 Q7ZUE4	Q7ZUE4 brachydanio
20	54	58.7	910	2 Q6FN08	Q6FN08 candida gla
21	53.5	58.2	212	1 PF11 PIG	P51524 sus scrofa
22	53.5	58.2	228	1 PF12 PIG	P51525 sus scrofa
23	53.5	58.2	902	2 Q9DBK8	Q9DBK8 mus musculu
24	53.5	58.2	941	2 Q91W60	Q91W60 mus musculu
25	53.5	58.2	941	2 Q8C7K5	Q8C7K5 mus musculu
26	53.5	58.2	942	2 Q54882	Q54882 mus musculu
27	53.5	58.2	942	2 Q8C7G9	Q8C7G9 mus musculu
28	53	57.6	121	2 Q6ZH25	Q6ZH25 oryza sativ
29	53	57.6	454	2 Q91Z39	Q91Z39 mus musculu
30	53	57.6	548	2 Q6ESK7	Q6ESK7 oryza sativ
31	53	57.6	552	2 Q76861	Q76861 drosophila

32 53 57.6 741 2 O15999 015999 ciona savig
33 53 57.6 1029 2 Q9YMX0 Q9YMX0 lymantria d
34 52.5 57.1 678 2 Q653U4 Q653U4 oryza sativ
35 52 56.5 134 2 Q9XIP3 Q9XIP3 arabidopsis
36 52 56.5 195 2 Q6ZWB3 Q6ZWB3 homo sapien
37 52 56.5 236 2 Q657Y0 Q657Y0 oryza sativ
38 52 56.5 388 2 Q8T8N6 Q8T8N6 caenorhabdi
39 52 56.5 398 2 Q17352 Q17352 caenorhabdi
40 52 56.5 541 2 Q7RYV7 Q7RYV7 neurospora
41 52 56.5 788 2 Q6PI09 Q6PI09 homo sapien
42 52 56.5 858 2 Q8NCZ1 Q8NCZ1 homo sapien
43 52 56.5 871 2 Q6NWC9 Q6NWC9 mus musculu
44 52 56.5 873 2 Q9WVC9 Q9WVC9 mus musculu
45 52 56.5 890 2 Q80W14 Q80W14 mus musculu

ALIGNMENTS

RESULT 1

PR39 PIG
ID PR39 PIG STANDARD; PRT; 172 AA.
AC P80054; Q9TR84; DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antibacterial protein PR-39 precursor.
GN Name=PR39;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95350216; PubMed=7624374;
RA Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,
RA Andersson L., Boman H.G.;
RT "Structure of the gene for porcine peptide antibiotic PR-39, a
RT cathelin gene family member: comparative mapping of the locus for the
RT human peptide antibiotic FALL-39";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=94071853; PubMed=8250863;
RA Storici P., Zanetti M.;
RT "A cDNA derived from pig bone marrow cells predicts a sequence
RT identical to the intestinal antibacterial peptide PR-39";
RL Biochem. Biophys. Res. Commun. 196:1058-1065(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=liver;
RX MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;
RA Zhao C., Ganz T., Lehrer R.I.;
RT "Structures of genes for two cathelin-associated antimicrobial
RT peptides: prophenin-2 and PR-39";
RL FEBS Lett. 376:130-134(1995).
RN [4]
RP SEQUENCE OF 131-169.
RC TISSUE=Intestine;
RX MEDLINE=92111534; PubMed=1765098;
RA Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
RA Matt V., Joernvall H.;
RT "Amino acid sequence of PR-39. Isolation from pig intestine of a new
RT member of the family of proline-arginine-rich antibacterial
RT peptides.";
RL Eur. J. Biochem. 202:849-854(1991).
RN [5]
RP SEQUENCE OF 131-164, AND FUNCTION.
RC TISSUE=Neutrophils;
RX MEDLINE=95088504; PubMed=7996056;
RA Shi J., Ross C.R., Chengappa M.M., Blecha F.;
RT "Identification of a proline-arginine-rich antibacterial peptide from

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RT  neutrophils that is analogous to PR-39, an antibacterial peptide from
RT  the small intestine.";
RL  J. Leukoc. Biol. 56:807-811(1994).
CC  -!- FUNCTION: Exerts a potent antimicrobial activity against both
CC  E.coli and B.megaterium.
CC  -!- TISSUE SPECIFICITY: Small intestine and bone marrow.
CC  -!- SIMILARITY: Belongs to the cathelicidin family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  -----
DR  EMBL; X87236; CAA60682.1; -.
DR  EMBL; L23825; AAA31109.1; -.
DR  EMBL; X89201; CAA61487.1; -.
DR  FIR; S68232; S68232.
DR  HSSP; P32196; 1KWI.
DR  InterPro; IPR001894; Cathelicidin.
DR  Pfam; PF00666; Cathelicidins; 1.
DR  ProDom; PD001838; Cathelicidins; 1.
DR  PROSITE; PS00946; CATHELICIDINS_1; 1.
DR  PROSITE; PS00947; CATHELICIDINS_2; 1.
DR  AmiDation; Antibiotic; Direct protein sequencing;
KW  Pyrrolidone carboxylic acid; Signal.
FT  SIGNAL 1 29 Potential.
FT  PROPEP 30 130 Antibacterial protein PR-39.
FT  CHAIN 131 169 Pyrrolidone carboxylic acid (By
FT  MOD_RES 30 30 similarity).
FT  DISULFID 85 96 By similarity.
FT  FT 107 124 By similarity.
FT  MOD_RES 169 169 Proline amide (G-170 provides amide
FT  group).
FT  CONFLICT 21 21 G -> A (in Ref. 2).
FT  CONFLICT 29 29 A -> T (in Ref. 1).
FT  CONFLICT 90 91 RQ -> QR (in Ref. 1).
FT  CONFLICT 117 119 IHS -> NDP (in Ref. 1).
FT  CONFLICT 157 157 P -> I (in Ref. 5).
FT  SEQUENCE 172 AA; 19476 MW; 994B792798C0E133 CRC64;
SQ
Query Match 100.0%; Score 92; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. NO. 0.0003;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGPPPPPPPPPP 15
DB 155 RPPGPPPPPPPPPP 169

RESULT 2
Q8ILQ0 PRELIMINARY; PRT; 484 AA.
ID Q8ILQ0;
AC Q8ILQ0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Spliceosome-associated protein, putative.
GN ORFNames=PF14_0194;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shalloom S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,

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RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
RL EMBL; AE014819; AAN36806.1; -.
DR HSSP; P11940; 1CVJ.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF00076; RRM_1; 2.
DR SMART; SMO0360; RRM; 2.
DR PROSITE; PS50102; RRM; 2.
DR PROSITE; PS50102; RRM; 2.
SQ SEQUENCE 484 AA; 53722 MW; 0858953D48F72E2B CRC64;

Query Match 72.8%; Score 67; DB 2; Length 484;
Best Local Similarity 76.9%; Pred. NO. 1.3;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPGPPPPPPPPPP 15
DB 429 PPGPPPNLPPNFP 441

RESULT 3
Q7RQAO PRELIMINARY; PRT; 415 AA.
ID Q7RQAO;
AC Q7RQAO;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Splicing factor 3b subunit 4.
GN Name=Py01202;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalloom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDAJ whole genome shotgun (WGS) entry which is
CC Preliminary data.
DR EMBL; AABL01000316; EAA20492.1; -.
DR HSSP; P11940; 1CVJ.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF00076; RRM_1; 2.
DR PROSITE; PS50102; RRM; 2.
DR PROSITE; PS50102; RRM; 2.
SQ SEQUENCE 415 AA; 46441 MW; 6D9D28AF80357B0A CRC64;

Query Match 68.5%; Score 63; DB 2; Length 415;
Best Local Similarity 76.9%; Pred. NO. 3.4;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPGPPPPPPPPPP 15
DB 350 PPPPPPTFPPTFP 362

RESULT 4

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081271 ID O81271 PRELIMINARY; PRT; 213 AA.
AC O81271;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Embryo-specific protein 3.
GN Name=AT53;
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Landsberg erecta;
RX MEDLINE=99308509; PubMed=10380802; DOI=10.1023/A:1006101404867;
RA Nuccio M.L., Thomas T.L.;
RT "AT51 and AT53: two novel embryo-specific genes in Arabidopsis
thaliana.";
RL Plant Mol. Biol. 39:1153-1163 (1999).
DR EMBL; AF067858; AAC27073.1; -
DR InterPro; IPR010417; AT53.
DR InterPro; IPR008976; PLAT LH2.
DR InterPro; IPR010916; TONE_Box_N.
DR Pfam; PF06232; AT53; 1.
DR PROSITE; PS00430; TONE DEPENDENT REC 1; UNKNOWN 1.
SQ SEQUENCE 213 AA; 23057 MW; DE745C727EDF8B34 CRC64;

Query Match 62.0%; Score 57; DB 2; Length 213;
Best Local Similarity 69.2%; Pred. No. 9.4;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PGCFPPRPFRPP 15
DB 161 PPHFPFPFPETP 173

RESULT 5
Q94K23 ID Q94K23 PRELIMINARY; PRT; 213 AA.
AC Q94K23;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Embryo-specific protein 3; AT53 (Embryo-specific protein 3).
GN Name=T28J14 130; Synonyms=At5g07190;
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF370461; AAK43838.1; -
DR EMBL; AY064694; AAL47396.1; -
DR InterPro; IPR010417; AT53.

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DR InterPro; IPR008976; PLAT LH2.
DR InterPro; IPR010916; TONE_Box_N.
DR Pfam; PF06232; AT53; 1.
DR PROSITE; PS00430; TONE DEPENDENT REC 1; UNKNOWN 1.
SQ SEQUENCE 213 AA; 23099 MW; DE74EACB1172834 CRC64;

Query Match 62.0%; Score 57; DB 2; Length 213;
Best Local Similarity 69.2%; Pred. No. 9.4;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PGCFPPRPFRPP 15
DB 161 PPHFPFPFPETP 173

RESULT 6
Q9LYP6 ID Q9LYP6 PRELIMINARY; PRT; 213 AA.
AC Q9LYP6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Embryo-specific protein 3 (AT53).
GN Name=T28J14 130;
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC EU Arabidopsis sequencing project;
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL163652; CAB87275.1; -
DR FIR; T48490; T48490.
DR InterPro; IPR010417; AT53.
DR InterPro; IPR008976; PLAT LH2.
DR InterPro; IPR010916; TONE_Box_N.
DR Pfam; PF06232; AT53; 1.
DR PROSITE; PS00430; TONE DEPENDENT REC 1; UNKNOWN 1.
SQ SEQUENCE 213 AA; 23083 MW; DE6230ACB1172834 CRC64;

Query Match 62.0%; Score 57; DB 2; Length 213;
Best Local Similarity 69.2%; Pred. No. 9.4;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PGCFPPRPFRPP 15
DB 161 PPHFPFPFPETP 173

RESULT 7
O61134 ID O61134 PRELIMINARY; PRT; 135 AA.
AC O61134;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE SP85 (Fragment).
GN Name=pspb;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS576;
RX MEDLINE=98367519; PubMed=9692967; DOI=10.1021/bi9808013;
RA Zhang Y., Brown R.D. Jr., West C.M.;

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RT "Two proteins of the Dictyostelium spore coat bind to cellulose in vitro.";

RL Biochemistry 37:10766-10779 (1998).

DR EMBL; AF066072; AAC19124.1; -.

FR DictyBase; DDB0185060; pspB.

FT NON_TER 1

FT NON_TER 135

SQ SEQUENCE 135 AA; 14829 MW; 500634A988A49408 CRC64;

Query Match 60.9%; Score 56; DB 2; Length 135;
Best Local Similarity 53.8%; Pred. No. 7.7;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGFPFRPPRPFP 15

||:|||||:

Db 38 PPSYPSPPTYP 50

RESULT 8

O61135

ID O61135 PRELIMINARY; PRT; 139 AA.

AC O61135;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE SP85 (Fragment).

GN Name=pspB;

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

OX NCBI_TaxID=44689;

RN [1]

SEQUENCE FROM N.A.

RP STRAIN=WS380B;

RX MEDLINE=98367519; PubMed=9692967; DOI=10.1021/bi9808013;

RA Zhang Y., Brown R.D. Jr., West C.M.;

RT "Two proteins of the Dictyostelium spore coat bind to cellulose in vitro.";

RL Biochemistry 37:10766-10779 (1998).

DR EMBL; AF066073; AAC19125.1; -.

FR DictyBase; DDB0185060; pspB.

FT NON_TER 1

FT NON_TER 139

SQ SEQUENCE 139 AA; 15368 MW; 4862D2F15137553P CRC64;

Query Match 60.9%; Score 56; DB 2; Length 139;
Best Local Similarity 53.8%; Pred. No. 8;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGFPFRPPRPFP 15

||:|||||:

Db 38 PPSYPSPPTYP 50

RESULT 9

Q67VV4

ID Q67VV4 PRELIMINARY; PRT; 150 AA.

AC Q67VV4;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Hypothetical protein OSUNBa0023122.10 (Hypothetical protein

DE P0530H05.25).

GN Name=OSUNBa0023122.10; Synonyms=P0530H05.25;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

SEQUENCE FROM N.A.

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC

clone:OSUNBa0023122.";

RL Submitted (FEB-2002) to the EMBL/GenBank/DBDJ databases.
RN [2]

RP SEQUENCE FROM N.A.

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC

clone:P0530H05.";

RL Submitted (APR-2001) to the EMBL/GenBank/DBDJ databases.

DR EMBL; AP004733; BAD37715.1; -.

DR EMBL; AP003541; BAD37390.1; -.

KW Hypothetical protein.

SQ SEQUENCE 150 AA; 16041 MW; 2C1B2FB6B092D311 CRC64;

Query Match 60.9%; Score 56; DB 2; Length 150;
Best Local Similarity 66.7%; Pred. No. 8.7;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RIPGFPFRPPRPFP 15

|||||

Db 62 RLPGLPFRPPRPFP 76

RESULT 10

O6Z4P0

ID Q6Z4P0 PRELIMINARY; PRT; 150 AA.

AC Q6Z4P0;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein OSUNBa0060017.6.

GN Name=OSUNBa0060017.6;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

SEQUENCE FROM N.A.

RA Sasaki T., Matsumoto T., Katayose Y.;

RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC

clone:OSUNBa0060017.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DBDJ databases.

DR EMBL; AP005167; BAC83800.1; -.

KW Hypothetical protein.

SQ SEQUENCE 150 AA; 15983 MW; 31ADE779971F0350 CRC64;

Query Match 60.9%; Score 56; DB 2; Length 150;
Best Local Similarity 66.7%; Pred. No. 8.7;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RIPGFPFRPPRPFP 15

|||||

Db 62 RLPGLPFRPPRPFP 76

RESULT 11

WNK1_HUMAN

ID WNK1_HUMAN STANDARD; PRT; 2382 AA.

AC Q9H4A3; O15052; Q86WL5; Q8N673; Q9P1S9;

DT 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Serine/threonine-protein kinase WNK1 (EC 2.7.1.37) (Protein kinase

DE with no lysine 1) (Protein kinase, lysine-deficient 1) (Kinase

DE deficient protein).

GN Name=PRKNK1; Synonyms=KDP, KIAA0344;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND CHROMOSOMAL

LOCATION.

RP TISSUE=Heart;

RX MEDLINE=21455683; PubMed=11571656; DOI=10.1038/sj/onc/1204726;
RA Verissimo E., Jordan P.;
RT "WNK kinases, a novel protein kinase subfamily in multi-cellular
RL organisms.";
RN Oncogene 20:5562-5569 (2001).
[2]
RN SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
RP
RC TISSUE=Kidney;
RX PubMed=14645531; DOI=10.1128/MCB.23.24.9208-9221.2003;
RA Delaloy C., Lu J., Houot A.M., Disse-Nicodeme S., Gasc J.M.,
RC Corvol P., Jeunemaitre X.;
RA "Multiple promoters in the WNK1 gene: one controls expression of a
RT kidney-specific kinase-defective isoform.";
RL Mol. Cell. Biol. 23:9208-9221 (2003).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 3).
RP
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RC Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[4]
RN SEQUENCE OF 1-670 FROM N.A. (ISOFORM 1/2), FUNCTION, SUBCELLULAR
RP LOCATION, AND TISSUE SPECIFICITY.
RC
RX TISSUE=Breast carcinoma;
RX MEDLINE=20127920; PubMed=10606000; DOI=10.1074/jbc.275.6.4311;
RA Moore T.M., Garg R., Johnson C., Ooptcoat M.J., Ridley A.J.,
RA Morris J.D.H.;
RT "PSK, a novel STE20-like kinase derived from prostatic carcinoma that
RT activates the JNK MAPK pathway and regulates actin cytoskeletal
RT organisation.";
RL J. Biol. Chem. 275:4311-4322 (2000).
[5]
RN SEQUENCE OF 69-2382 FROM N.A. (ISOFORM 2).
RP
RC TISSUE=Brain;
RX MEDLINE=97349984; PubMed=9205841;
RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. VII.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 4:141-150 (1997).
[6]
RN REVISIONS TO N-TERMINUS.
RP
RX MEDLINE=22158633; PubMed=12168954;
RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
RT "Construction of expression-ready cDNA clones for KIAA genes: manual
RT curation of 330 KIAA cDNA clones.";
RL DNA Res. 9:99-106 (2002).
[7]
RN DISEASE.
RP
RX MEDLINE=21390047; PubMed=11498583; DOI=10.1126/science.1062844;
RA Wilson F.H., Disse-Nicodeme S., Choate K.A., Ishikawa K.,
RA Nelson-Williams C., Desitter I., Gunel M., Milford D.V., Lipkin G.W.,
RA Achard J.M., Feely M.P., Dussol B., Berland Y., Unwin R.J., Mayan H.,
RA Simon D.B., Farfel Z., Jeunemaitre X., Lifton R.P.;

RT "Human hypertension caused by mutations in WNK kinases.";
RL Science 293:1107-1112 (2001).
CC -!- FUNCTION: Controls sodium and chloride ion transport by inhibiting
CC the activity of PRKNK4, potentially by either phosphorylating the
CC kinase or via an interaction between PRKNK4 and the
CC autoinhibitory domain of PRKNK1. PRKNK4 regulates the activity
CC of the thiazide-sensitive Na-Cl cotransporter, SLC12A3, by
CC phosphorylation. PRKNK1 may also play a role in actin
CC cytoskeletal reorganization.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- COFACTOR: Magnesium.
CC -!- ENZYME REGULATION: By hypertonicity. Activation requires
CC autophosphorylation of Ser-382. Phosphorylation of Ser-378 also
CC promotes increased activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative promoter;
CC Comment=2 isoforms, 1 (shown here) and 4, are produced by use of
CC alternative promoters;
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q9H4A3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9H4A3-2; Sequence=VSP_050638;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=Q9H4A3-3; Sequence=VSP_050635, VSP_050636;
CC Name=4; Synonyms=Kidney-specific, Kinase-defective;
CC IsoId=Q9H4A3-4; Sequence=VSP_050634, VSP_050637;
CC -!- TISSUE SPECIFICITY: Widely expressed, with highest levels observed
CC in the testis, heart, kidney and skeletal muscle.
CC -!- DISBAS: Defects in PRKNK1 are a cause of pseudohypoadosteronism
CC type II (PHAII) [MIM:145260]. PHAII is an autosomal dominant
CC disease characterized by severe hypertension, hyperkalemia, and
CC sensitivity to thiazide diuretics which may result from a chloride
CC shunt in the renal distal nephron.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. WNK
CC subfamily.
CC -!- CAUTION: Cys-250 is present instead of the conserved Lys which is
CC expected to be an active site residue. Lys-233 appears to fulfill
CC the required catalytic function.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; AJ296290; CAC15059.1; -
CC EMBL; AY231477; AAO46160.1; -
CC EMBL; BC021121; AAF31483.1; -
CC EMBL; AF061944; AAF31483.1; -
CC EMBL; AB002342; BAA20802.2; -
CC Genew; HGNC:14540; PRKNK1.
CC MIM; 605232; -
CC MIM; 145260; -
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005524; F:ATP binding; IDA.
CC GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
CC GO; GO:0006811; P:ion transport; ISS.
CC GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
CC GO; GO:0007243; P:protein kinase cascade; IDA.
CC GO; GO:0050794; P:regulation of cellular process; ISS.
CC InterPro; IPR011009; Kinase-like.
CC InterPro; IPR008271; Ser_thr_kinase.
CC Pfam; PF00069; Pkinase; I.
CC ProDom; PD000001; Proc_kinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Alternative promoter usage; Alternative splicing; ATP-binding;
 KW Phosphorylation; Protein kinase inhibitor;
 KW Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 221 479 Protein kinase.
 FT NP_BIND 227 235 ATP (By similarity).
 FT BINDING 233 233 ATP (By similarity).
 FT ACT_SITE 349 349 Proton acceptor (By similarity).
 FT MOD_RES 378 378 Phosphoserine (by autocatalysis) (By similarity).
 FT MOD_RES 382 382 Phosphoserine (by autocatalysis) (By similarity).
 FT VARSPLIC 1 407 Missing (in isoform 4).
 FT VARSPLIC 386 393 /FTID-VSP_050634.
 FT VARSPLIC 394 2382 /TFEWAPE -> MFQVILGA (in isoform 3).
 FT VARSPLIC 408 437 /FTID-VSP_050635.
 FT VARSPLIC 792 1037 /FTID-VSP_050636.
 FT CONFLICT 669 670 FCGMCLWATSPYVSEQNAAQIVRRVTS -> MDIKKKD
 FT CONFLICT 740 740 Missing (in isoform 2).
 FT CONFLICT 1808 1808 VS -> GG [in Ref. 4].
 FT CONFLICT 1836 1836 I -> M (in Ref. 5).
 FT CONFLICT 1836 1836 Missing (in Ref. 5).
 SQ SEQUENCE 2382 AA; 250755 MW; ADDA6C86554B7FCA CRC64;

Query Match 60.9%; Score 56; DB 1; Length 2382;
 Best Local Similarity 72.7%; Pred No. 1.7e+02;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GFPPRPFRPP 15
 DB 945 GFPPRLPPQVP 955

RESULT 12

Q9UPH5 PRELIMINARY; PRT; 393 AA.
 AC Q9UPH5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE Dynamin II (AA 474-866) (Fragment).
 GN Name=DNM2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCready P.M., Skowronski E., Richardson P.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Sakaleas G., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Scott D.,
 RA Danganan L., Eriar A., Christensen M., Georgescu A., Avila J.,
 RA Attix C., Andreise T., Truheim M., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RL Nat. Genet. 16:40-45 (2004).
 CC -!- SIMILARITY: Contains 1 PH domain.
 DR EMBL; AC007229; AAD23603.1; -.
 DR HSSP; Q05193; 1DYN.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR InterPro; IPR003375; Dynamain_central.
 DR InterPro; IPR003130; GED.
 DR InterPro; IPR001849; PH.
 DR Pfam; PF01031; Dynamain_M; 1.
 DR Pfam; PF02212; GED; 1.
 DR Pfam; PF00169; PH; 1.

DR SMART; SM00302; GED; 1.
 DR SMART; SM00233; PH; 1.
 DR PROSITE; PS00003; PH DOMAIN; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 393 AA; 44036 MW; FAA7B8456023E2D1 CRC64;
 Query Match 59.8%; Score 55; DB 2; Length 393;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 RIPGFPFRPPRP 15
 DB 360 RIPGIPPGVSRPP 374
 RESULT 13
 Q8N1K8 PRELIMINARY; PRT; 464 AA.
 ID Q8N1K8;
 AC Q8N1K8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Hypothetical protein FLJ40556.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX PubMed14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshihara Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Moniyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Serba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs";
 RL Nat. Genet. 36:40-45 (2004).
 CC -!- SIMILARITY: Contains 1 PH domain.
 DR EMBL; AK097875; BAC05190.1; -.
 DR HSSP; Q05193; 2DYN.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR InterPro; IPR000375; Dynamain_central.
 DR InterPro; IPR003130; GED.
 DR InterPro; IPR001849; PH.
 DR Pfam; PF01031; Dynamain_M; 1.
 DR Pfam; PF02212; GED; 1.
 DR Pfam; PF00169; PH; 1.

DR Pfam; PF00169; PH; 1.
 DR SMART; SM00302; GED; 1.
 DR SMART; SM00233; PH; 1.
 DR PROSITE; PS00003; PH_DOMAIN; 1.
 SQ SEQUENCE 464 AA; 52198 MW; A56592DDAD9B7368 CRC64;

Query Match 59.8%; Score 55; DB 2; Length 464;
 Best Local Similarity 66.7%; Pred. No. 39;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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 Db 431 RIPPFGPPGVPSP 445

RESULT 14
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 AC P50570; Q725S3; Q9UPH9;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE DYNamin 2 (EC 3.6.5.5).
 GN Name=DNM2; Synonyms=DYN2;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=9601162; PubMed=7590285; DOI=10.1016/0378-1119(95)00275-B;
 RA Diatloff-Zito C., Gordon A.J.E., Duchaud E., Merlin G.;
 RT "Isolation of an ubiquitously expressed cDNA encoding human dynamin
 II, a member of the large GTP-binding protein family.";
 RL Gene 163:301-306(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX PubMed=15057824; DOI=10.1038/nature02399;
 RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
 RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
 RA Aerts A., Alther M., Ashworth L., Bajorek E., Black S., Branscomb E.,
 RA Caenepeel S., Carrano A.V., Caolile C., Chan Y.M., Christensen M.,
 RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C.,
 RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,
 RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
 RA Haydu L., Ho I., Huang W., Israeli S., Jett J., Kadner K., Kimball H.,
 RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
 RA Malfatti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,
 RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
 RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
 RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
 RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
 RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
 RA Purey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
 RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
 RA Rubin E.M., Lucas S.M.;
 RA "The DNA sequence and biology of human chromosome 19.";
 RL Nature 428:529-535(2004).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Uterus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins R.D., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Hopkins R.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong F.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP INTERACTION WITH SHANK PROTEINS.
 RX MEDLINE=21611185; PubMed=11583995; DOI=10.1074/jbc.M104927200;
 RA Okamoto P.M., Gamby C., Wells D., Fallon J., Vallee R.B.;
 RT "Dynamin isoform-specific interaction with the shank/proSAP
 scaffolding proteins of the postsynaptic density and actin
 cytoskeleton.";
 RL J. Biol. Chem. 276:48458-48465(2001).
 CC -!- FUNCTION: Microtubule-associated force-producing protein involved
 in producing microtubule bundles and able to bind and hydrolyze
 GTP. Most probably involved in vesicular trafficking processes, in
 particular endocytosis.
 CC -!- CATALYTIC ACTIVITY: GTP + H(2)O = GDP + phosphate.
 CC -!- SUBUNIT: Interacts with SHANK1 and SHANK2.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Microtubule-associated. Also
 found in the postsynaptic density of neuronal cells.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoID=P50570-1; Sequence=Displayed;
 CC Name=2;
 CC IsoID=P50570-2; Sequence=VSP_001325;
 CC -!- TISSUE SPECIFICITY: Ubiquitously expressed.
 CC -!- SIMILARITY: Belongs to the dynamin family.
 CC -!- SIMILARITY: Contains 1 PH domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L36983; AAA88025.1; --
 CC EMBL: AC007229; RAD23604.1; --
 CC EMBL: BC054501; AAH54501.1; --
 CC HSSP: Q05193; 2DYN.
 CC IntAct; P50570; --
 CC GeneW; HGNC:2974; DNM2.
 CC MIM: 602378; --
 CC GO: GO:0000086; P:G2/M transition of mitotic cell cycle; TAS.
 CC InterPro: IPR001401; Dynamin.
 CC InterPro: IPR000375; Dynamin_central.
 CC InterPro: IPR003130; GED.
 CC InterPro: IPR001849; PH.
 CC Pfam: PF01031; Dynamin_M; 1.
 CC Pfam: PF00350; Dynamin_N; 1.
 CC Pfam: PF02212; GED; 1.
 CC Pfam: PF00169; PH; 1.
 CC PRINTS; PR00195; DYNAMIN.
 CC SMART; SM00053; DYNC; 1.
 CC SMART; SM00302; GED; 1.
 CC SMART; SM00233; PH; 1.
 CC PROSITE; PS00410; DYNAMIN; 1.
 CC PROSITE; PS00003; PH_DOMAIN; 1.
 CC Alternative splicing; Endocytosis; GTP-binding; Hydrolase;
 KW Microtubule; Motor protein; Multigene family.
 FT NP_BIND 38 45 GTP (By similarity).
 FT NP_BIND 136 140 GTP (By similarity).
 FT NP_BIND 205 208 GTP (By similarity).
 FT DOMAIN 519 625 PH.
 FT VARSPLIC 516 519 Missing (in isoform 2).
 FT /FTid=VSP_001325.

Job time : 53.9545 secs

FT CONFLICT 155 156 QI -> RV (in Ref. 1).
FT CONFLICT 316 316 N -> I (in Ref. 1).
FT CONFLICT 324 324 R -> P (in Ref. 1).
SQ SEQUENCE 870 AA; 98063 MW; 2F4567B75980935D CRC64;

Query Match 59.8%; Score 55; DB 1; Length 870;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RPPGFPFRFPFRFP 15

DB 837 RPPGIPGVPSRRP 851

RESULT 15

Q7SHV3
ID Q7SHV3 PRELIMINARY; PRT; 213 AA.
AC Q7SHV3;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU02508.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Meves W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Maucelli E., Bieleke C., Rudd S., Frishman D.,
RA Kryatofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX01000002; EAA36403.1; -.
DR HSP; P14678; ID3B.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IEA.
DR GO; GO:0008248; F:pre-mRNA splicing factor activity; IEA.
DR GO; GO:0006397; P:mRNA processing; IEA.
DR InterPro; IPR010920; Sm like riboprot.
DR InterPro; IPR006649; snRNP.
DR InterPro; IPR001163; snRNP_Sm.
DR Pfam; PF01423; LSM; 1.
DR ProDom; PD020287; snRNP; 1.
KW Hypothetical protein.
SQ SEQUENCE 213 AA; 21440 MW; 17356AF1B36F2240 CRC64;

Query Match 59.2%; Score 54.5; DB 2; Length 213;
Best Local Similarity 45.8%; Pred. No. 19;
Matches 11; Conservative 0; Mismatches 2; Indels 11; Gaps 1;

QY 3 PPGFP-----PRFPFRFP 15

DB 174 PPGFVFPAGPAGPAGPAGPAGPAGP 197

Search completed: October 26, 2005, 05:18:37

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:02:04 ; Search time 15.4091 Seconds
(without alignments)
72.667 Million cell updates/sec

Title: US-10-014-147-6

Perfect score: 92

Sequence: 1 RIPPFPFPPPPRFP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/protdata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/protdata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/protdata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/protdata/1/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/protdata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	15	4	US-08-930-777A-6
2	92	100.0	39	1	US-08-162-052-1
3	92	100.0	39	1	US-08-310-722-1
4	92	100.0	39	2	US-08-419-066-1
5	92	100.0	39	2	US-08-728-333-1
6	92	100.0	39	3	US-09-024-975-1
7	92	100.0	39	4	US-08-930-777A-1
8	92	100.0	39	5	PCT-US95-12080-1
9	75.5	82.1	38	4	US-09-739-535-1
10	57.5	62.5	78	1	US-08-487-359-5
11	57.5	62.5	78	1	US-08-222-798A-5
12	57	62.0	16	3	US-09-024-975-3
13	57	62.0	16	4	US-08-930-777A-5
14	57	62.0	23	4	US-08-930-777A-3
15	57	62.0	26	2	US-08-419-066-2
16	57	62.0	26	3	US-09-024-975-2
17	57	62.0	26	4	US-08-930-777A-2
18	56	60.9	741	4	US-09-854-856-60
19	56	60.9	769	4	US-09-854-856-44
20	56	60.9	801	4	US-09-854-856-28
21	56	60.9	829	4	US-09-854-856-12
22	56	60.9	894	4	US-09-854-856-54
23	56	60.9	922	4	US-09-854-856-38
24	56	60.9	954	4	US-09-854-856-22
25	56	60.9	982	4	US-09-854-856-6
26	56	60.9	2004	4	US-09-854-856-58
27	56	60.9	2032	4	US-09-854-856-42

28 56 60.9 2064 4 US-09-854-856-26 Sequence 26, Appl
29 56 60.9 2092 4 US-09-854-856-10 Sequence 10, Appl
30 56 60.9 2141 4 US-09-854-856-56 Sequence 56, Appl
31 56 60.9 2157 4 US-09-854-856-52 Sequence 52, Appl
32 56 60.9 2169 4 US-09-854-856-40 Sequence 40, Appl
33 56 60.9 2185 4 US-09-854-856-36 Sequence 36, Appl
34 56 60.9 2201 4 US-09-854-856-24 Sequence 24, Appl
35 56 60.9 2217 4 US-09-854-856-20 Sequence 20, Appl
36 56 60.9 2229 4 US-09-854-856-8 Sequence 8, Appl
37 56 60.9 2245 4 US-09-854-856-4 Sequence 4, Appl
38 56 60.9 2294 4 US-09-854-856-50 Sequence 50, Appl
39 56 60.9 2322 4 US-09-854-856-34 Sequence 34, Appl
40 56 60.9 2354 4 US-09-854-856-18 Sequence 18, Appl
41 56 60.9 2382 4 US-09-854-856-2 Sequence 2, Appl
42 55 59.8 866 4 US-09-949-016-6568 Sequence 6568, Ap
43 55 59.8 870 4 US-09-538-092-1168 Sequence 1168, Ap
44 53.5 58.2 79 1 US-08-487-359-1 Sequence 1, Appl
45 53.5 58.2 79 1 US-08-487-359-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-930-777A-6
; Sequence 6, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-930-777A-6

Query Match 100.0%; Score 92; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIPPFPFPPPPRFP 15
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Db      1 R1PPGFPFRPPRFP 15

RESULT 2
US-08-162-052-1
; Sequence 1, Application US/08162052
; Patent No. 5485575
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong-Youn
; APPLICANT: BOWAN, Hans G
; APPLICANT: MUTT, Viktor
; APPLICANT: JORNVAL, Hans
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,052
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9101838-2
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92-22578
; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 003300-299
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-162-052-1

Query Match      100.0%; Score 92; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 R1PPGFPFRPPRFP 15
       |||||
Db      25 R1PPGFPFRPPRFP 39

RESULT 3
US-08-310-722-1
; Sequence 1, Application US/08310722
; Patent No. 5654273
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800

Query Match      100.0%; Score 92; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 R1PPGFPFRPPRFP 15
       |||||
Db      25 R1PPGFPFRPPRFP 39

RESULT 4
US-08-419-066-1
; Sequence 1, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 23625
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-419-066-1

Query Match 100.0%; Score 92; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGPPPPPPRFP 15
DB 25 RPPGPPPPPPRFP 39

RESULT 5
US-08-728-333-1
Sequence 1, Application US/08728333
Patent No. 5863897
GENERAL INFORMATION:
APPLICANT: Gallo, Richard L.
APPLICANT: Klagsbrun, Michael
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,333
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,722
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: CMCC379
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
PUBLICATION INFORMATION:

AUTHORS: Lee, Jong-Youn
AUTHORS: Boman, Hans G.
AUTHORS: Mutt, Viktor
AUTHORS: Jorvall, Hans
TITLE: No. 5863897el Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-728-333-1
Query Match 100.0%; Score 92; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGPPPPPPRFP 15
DB 25 RPPGPPPPPPRFP 39

RESULT 6
US-09-024-975-1
Sequence 1, Application US/09024975
Patent No. 6133233
GENERAL INFORMATION:
APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: BLECHA, FRANK
APPLICANT: SHI, JISHU
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/802,306
FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25585-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-975-1

Query Match 100.0%; Score 92; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGPPPPPPRFP 15
DB 25 RPPGPPPPPPRFP 39

RESULT 7

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US-08-930-777A-1
; Sequence 1, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-930-777A-1

Query Match 100.0%; Score 92; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRPPRPFP 15
Db 25 RPPGFPFRPPRPFP 39

RESULT 8
US-09-739-535-1
; Sequence 1, Application PC/TUS9512080
; GENERAL INFORMATION:
; APPLICANT: Children's Medical Center Corporaton
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

US-09-739-535-1
; Sequence 1, Application US/09739535
; Patent No. 6794490
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/739,535
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PPT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-739-535-1

Query Match 82.1%; Score 75.5; DB 4; Length 38;
Best Local Similarity 93.3%; Pred. No. 0.0035;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 RPPGFPFRPPRPFP 15
Db 25 RIPP-FPPRFPFPFP 38

RESULT 10
US-08-487-359-5
; Sequence 5, Application US/08487359
; Patent No. 5633229
; GENERAL INFORMATION:
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: LEHRER, ROBERT I.
; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
; NUMBER OF SEQUENCES: 9

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 2000 Pennsylvania Ave. N.W.
;; CITY: Washington, D.C.
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 20006-1812
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/487,359
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/222,798
;; FILING DATE: 05-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MURASHIGE, KATE H.
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 2000-0553.00
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 887-1500
;; TELEFAX: (202) 887-0763
;; TELEX: 90-4030
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 78 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-487-359-5

Query Match 62.5%; Score 57.5; DB 1; Length 78;
Best Local Similarity 78.6%; Pred. No. 1.2;
Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 PPGFPP-PRFPFPP 15
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Db 34 PPGFPP-PRFPFPP 47

RESULT 11
US-08-222-798A-5
; Sequence 5, Application US/08222798A
; Patent No. 5804553
; GENERAL INFORMATION:
; APPLICANT: KORRYAKOV, VLADIMIR N.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: LEHRER, ROBERT I.
; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington, D.C.
; STATE: CA
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,798A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959

;; REFERENCE/DOCKET NUMBER: 2000-0553.00
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 887-1500
;; TELEFAX: (202) 887-0763
;; TELEX: 90-4030
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 78 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-222-798A-5

Query Match 62.5%; Score 57.5; DB 1; Length 78;
Best Local Similarity 78.6%; Pred. No. 1.2;
Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 PPGFPP-PRFPFPP 15
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Db 34 PPGFPP-PRFPFPP 47

RESULT 12
US-09-024-975-3
; Sequence 3, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-024-975-3

Query Match 62.0%; Score 57; DB 3; Length 16;
Best Local Similarity 76.9%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPPGFPFPPRPP 13
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Db 3 RPPGFPFPPRPP 15

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-930-777A-3

Query Match 62.0%; Score 57; DB 4; Length 23;
Best Local Similarity 76.9%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 3; Indels

QY 1 RPPGPPPRFPPR 13
| | | | |
Db 10 RPPPPFPPRLPPR 22

RESULT 15
US-08-419-066-2
Sequence 2, Application US/08419066
Patent No. 583093
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Shi, Jiehu
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: John M. Collins, Hovey, Williams, Timmons &
ADDRESSER: Collins
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,066
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 23625
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-2

Query Match      62.0%; Score 57; DB 2; Length 26;
Best Local Similarity 76.9%; Pred. No. 0.47;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RPPGPPPPPPPPR 13
      | | | | | | | |
Db      13 RPPPPPPRLPPR 25

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Job time : 16.4091 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 05:05:05 ; Search time 55.3636 Seconds
(without alignments)
113.119 Million cell updates/sec

Title: US-10-014-147-6

Perfect score: 92

Sequence: 1 RPPGFPFPFPFRFP 15

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	92	100.0	15	US-10-651-147-6	Sequence 6, Appli
3	92	100.0	39	US-10-014-147-1	Sequence 1, Appli
4	92	100.0	39	US-10-391-155-1	Sequence 1, Appli
5	92	100.0	39	US-10-391-155-2	Sequence 2, Appli
6	92	100.0	39	US-10-391-155-6	Sequence 1, Appli
7	92	100.0	39	US-10-651-147-1	Sequence 6, Appli
8	92	100.0	42	US-10-344-709C-18	Sequence 18, Appl
9	92	100.0	42	US-10-916-185-14	Sequence 14, Appl
10	92	100.0	42	US-10-991-286A-44	Sequence 44, Appl
11	92	100.0	42	US-11-004-379-20	Sequence 20, Appl

12	75.5	82.1	38	9	US-09-738-742-1	Sequence 1, Appli
13	75.5	82.1	38	9	US-09-739-535-1	Sequence 1, Appli
14	60	65.2	103	15	US-10-424-599-258982	Sequence 258982,
15	59	64.1	103	15	US-10-424-599-211799	Sequence 211799,
16	59	64.1	107	15	US-10-424-599-208016	Sequence 208016,
17	58.5	63.6	101	16	US-10-425-115-322756	Sequence 322756,
18	57.5	62.0	366	16	US-10-408-765A-1261	Sequence 1261, Ap
19	57	62.0	16	14	US-10-014-147-5	Sequence 5, Appli
20	57	62.0	16	15	US-10-651-147-3	Sequence 3, Appli
21	57	62.0	23	14	US-10-014-147-3	Sequence 3, Appli
22	57	62.0	23	15	US-10-651-147-3	Sequence 2, Appli
23	57	62.0	26	14	US-10-014-147-2	Sequence 2, Appli
24	57	62.0	26	15	US-10-651-147-2	Sequence 2, Appli
25	56	60.9	125	16	US-10-437-963-113302	Sequence 113302,
26	56	60.9	153	16	US-10-425-115-268716	Sequence 268716,
27	56	60.9	304	14	US-10-156-761-13550	Sequence 13550, A
28	56	60.9	560	13	US-10-114-893-84	Sequence 84, Appl
29	56	60.9	615	16	US-10-425-115-319541	Sequence 319541,
30	56	60.9	2382	14	US-10-196-935A-2	Sequence 2, Appli
31	56	60.9	2382	15	US-10-052-648A-40	Sequence 40, Appl
32	56	60.9	2382	15	US-10-336-472-230	Sequence 230, App
33	56	60.9	2382	16	US-10-408-765A-1404	Sequence 1404, Ap
34	56	60.9	2382	20	US-11-009-554-8	Sequence 8, Appli
35	55.5	60.3	111	16	US-10-425-115-195600	Sequence 195600,
36	55	59.8	83	16	US-10-437-963-118176	Sequence 118176,
37	55	59.8	96	16	US-10-437-963-120965	Sequence 120965,
38	55	59.8	117	16	US-10-425-115-230243	Sequence 230243,
39	55	59.8	143	15	US-10-424-599-189499	Sequence 189499,
40	55	59.8	171	16	US-10-437-963-111951	Sequence 111951,
41	55	59.8	228	16	US-10-767-701-43436	Sequence 43436, A
42	55	59.8	380	10	US-09-955-999-82	Sequence 82, Appl
43	54	58.7	103	16	US-10-437-963-136312	Sequence 136312,
44	53.5	58.2	122	15	US-10-424-599-193533	Sequence 193533,
45	53	57.6	107	16	US-10-437-963-164555	Sequence 164555,

ALIGNMENTS

RESULT 1
US-10-014-147-6
; Sequence 6, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A


```

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-391-155-2
Query Match 100.0%; Score 92; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGPPPPPPRFP 15
DB 25 RPPGPPPPPPRFP 39
|||||
|||||

RESULT 6
US-10-391-155-6
; Sequence 6, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated
; selective inhibition of IKGA degradation
;
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: WordPerfect version 10
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-044/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-391-155-6
Query Match 100.0%; Score 92; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGPPPPPPRFP 15
DB 25 RPPGPPPPPPRFP 39
|||||
|||||

RESULT 7
US-10-651-147-1
; Sequence 1, Application US/10651147
; Publication No. US20040043934A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide

```



```

; PRIOR APPLICATION NUMBER: PCT/US2004/18271
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/476,947
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptide
US-10-991-286A-44

Query Match      100.0%; Score 92; DB 18; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RPPGPPPPPPPPPP 15
      |||||
Db      25 RPPGPPPPPPPPPP 39

RESULT 11
US-11-004-379-20
; Sequence 20, Application US/11004379
; Publication No. US20050153337A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: iRNA CONJUGATES
; FILE REFERENCE: 14174-087001
; CURRENT APPLICATION NUMBER: US/11/004,379
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: PCT/US04/10586
; PRIOR FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 60/460,783
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/462,894
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptides
US-11-004-379-20

Query Match      100.0%; Score 92; DB 20; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RPPGPPPPPPPPPP 15
      |||||
Db      25 RPPGPPPPPPPPPP 39

US-10-738-742-1
; Sequence 1, Application US/09738742
; Publication No. US20020025924A1
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/738,742
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-738-742-1

Query Match      82.1%; Score 75.5; DB 9; Length 38;
Best Local Similarity 93.3%; Pred. No. 0.039;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 RPPGPPPPPPPPPP 15
      |||||
Db      25 RPPGPPPPPPPPPP 38

RESULT 13
US-09-739-535-1
; Sequence 1, Application US/09739535
; Publication No. US20020058785A1
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/739,535
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-739-535-1

Query Match      82.1%; Score 75.5; DB 9; Length 38;
Best Local Similarity 93.3%; Pred. No. 0.039;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 RPPGPPPPPPPPPP 15
      |||||
Db      25 RPPGPPPPPPPPPP 38

RESULT 14
US-10-424-599-258982
; Sequence 258982, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
```

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; SEQ ID NO 258982
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_75885C.1.pep
US-10-424-599-258982

Query Match      65.2%; Score 60; DB 15; Length 103;
Best Local Similarity 66.7%; Pred. No. 6.3;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 RPPGFPFPPRP 15
      |:| ||| |||
DB      85 RVPRVPPRP 99

RESULT 15
US-10-424-599-211799
; Sequence 211799, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 211799
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_33281C.1.pep
US-10-424-599-211799

Query Match      64.1%; Score 59; DB 15; Length 103;
Best Local Similarity 78.6%; Pred. No. 8.2;
Matches 11; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY      3 PPGFP--PRFP 14
      ||||| |||
DB      27 PPGFPWPRI 40

Search completed: October 26, 2005, 05:28:58
Job time : 56.3636 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:51:43 ; Search time 55.1091 Seconds
(without alignments)
98.253 Million cell updates/sec

Title: US-10-014-147-7

Perfect score: 83

Sequence: 1 RRRPRPPYLRPRP 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp19808:*

2: Geneseqp19908:*

3: Geneseqp20008:*

4: Geneseqp20018:*

5: Geneseqp20028:*

6: Geneseqp20038:*

7: Geneseqp20048:*

8: Geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	14	2 AAW01450	Aaw01450 Leukocyte
2	83	100.0	14	2 AAW75725	Aaw75725 Proline/A
3	83	100.0	14	8 ADE86118	Ade86118 Proline-a
4	83	100.0	14	8 ADL67260	Adl67260 Antimicro
5	83	100.0	15	3 AAB26885	Aab26885 PR-39 der
6	83	100.0	15	4 AAB97277	Aab97277 PR-39 der
7	83	100.0	15	4 AAB84691	Aab84691 Amino aci
8	83	100.0	19	2 AAW01452	Aaw01452 Leukocyte
9	83	100.0	19	8 ADE86115	Ade86115 Proline-a
10	83	100.0	19	8 ADL67257	Adl67257 Antimicro
11	83	100.0	26	2 AAW01447	Aaw01447 Leukocyte
12	83	100.0	26	2 AAW75723	Aaw75723 Proline/A
13	83	100.0	26	8 ADE86113	Ade86113 Proline-a
14	83	100.0	26	8 ADL67255	Adl67255 Antimicro
15	83	100.0	39	2 AAR30491	Aar30491 Antibacte
16	83	100.0	39	2 AAR99121	Aar99121 Magainin
17	83	100.0	39	2 AAR94446	Aar94446 Synducin
18	83	100.0	39	2 AAW01446	Aaw01446 Leukocyte
19	83	100.0	39	2 AAW75722	Aaw75722 Proline/A
20	83	100.0	39	3 AAB26888	Aab26888 PR-39 pep
21	83	100.0	39	4 AAB97280	Aab97280 PR-39 pep
22	83	100.0	39	4 AAB84690	Aab84690 Amino aci
23	83	100.0	39	8 AAD35364	Aad35364 Antimicro
24	83	100.0	39	8 ADE86112	Ade86112 Proline-a
25	83	100.0	39	8 ADL67254	Adl67254 Antimicro

ALIGNMENTS

RESULT 1

AAW01450
ID AAW01450 standard; peptide; 14 AA.

XX
AC AAW01450;

XX
DT 18-JUN-1997 (first entry)

XX
DE Leukocyte O2- production inhibitor peptide PR14.

XX
KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
KW tissue damage; oxygen radical; inflammatory disease; therapy.

XX
OS Synthetic.

XX
PN WO9632129-A1.

XX
PD 17-OCT-1996.

XX
PF 10-APR-1996; 96WO-US004674.

XX
PR 10-APR-1995; 95US-00419066.

XX
PA (UNIV) UNIV KANSAS STATE RES FOUND.

XX
PI Blecha F, Shi J;

XX
PS WPI; 1996-476842/47.

XX
PT Inhibition of leukocyte superoxide anion prodn. and attraction of

XX
PR Leukocytes - using peptide(s) partic. based on antimicrobial PR-39.

XX
PS Claim 12; Page 28; 45pp; English.

XX
XX AAW01447-W01454 represent fragments of the proline-arginine rich
XX antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
XX isolated from porcine small intestine, and has also been identified in
XX human and porcine neutrophils. PR39 kills bacteria by interfering with
XX DNA and/or protein synthesis. PR39 also induces syndecan expression on
XX mesenchymal cells. Syndecans are important in wound repair, showing that
XX PR39 can be used in wound repair, as well as in antibacterial agents.
XX These sequences, and PR39, can be used in the method of the invention.
XX The method of the invention is for inhibiting leukocyte superoxide anion
XX (O2-) production. The method comprises administering to a leukocyte a
XX peptide (such as this sequence) capable of inhibiting leukocyte O2-

CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting tissue
 CC damage at the wound site caused by excessive oxygen radicals produced by
 CC these leukocytes. They can also be used to develop products for treating
 CC inflammatory disease states

XX Sequence 14 AA;
 SQ

Query Match 100.0%; Score 83; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RRP 14
 |||||
 Db 1 RRRPRPPYLP RRP 14

RESULT 2

AAW75725
 ID AAW75725 standard; peptide; 14 AA.

XX
 AC AAW75725;

DT 19-NOV-1998 (first entry)

DE Proline/Arginine rich peptide.

XX Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;
 KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;
 KW coronary bypass; organ transplantation surgery.

XX Synthetic.

XX WO9835690-A1.

XX 20-AUG-1998.

XX 17-FEB-1998; 98WO-US003207.

XX 18-FEB-1997; 97US-00802306.

XX 16-FEB-1998; 98US-00024975.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Ross CR, Blecha F, Shi J;

XX WPI; 1998-495359/42.

XX Reduction of reperfusion injury in temporarily occluded blood vessels -
 PT by administration of a peptide which is rich in proline or arginine
 PT residues.

XX Claim 3; Page 15; 35pp; English.

XX Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
 CC administration into a mammal's bloodstream reduce reperfusion injury
 CC (production of reactive oxygen species, neutrophil adherence to
 CC endothelium, and extravasation of neutrophils). These peptides have two
 CC requirements: they contain the consensus sequence PXXP, where P is a
 CC proline residue and X is any amino acid residue, which has been found to
 CC inhibit superoxide production, and secondly they have arginine residues
 CC adjacent to these motifs, required for effective inhibition. It was
 CC established by structural and function analysis that a peptide should
 CC ideally contain 4 or 6 of these motifs, and that inhibitory activity is
 CC correlated with the increase of length of peptides. The effectiveness of
 CC these peptides was determined by investigating the production of the
 CC neutrophil superoxide anion, and also the inhibition of neutrophil
 CC chemotaxis. From this, it was found that all of the peptides inhibited
 CC NADPH oxidase to some extent. All of the peptides also inhibit neutrophil
 CC oxidase activity. PR-39 is believed, to be the most potent endogenous
 CC down regulator of NADPH oxidase yet discovered, and from the data
 CC produced, it can be suggested to be involved in eliminating or reducing
 CC the reperfusion injury induced adhesion and extraction of neutrophils.

CC The peptides are also useful in connection with surgical procedures such
 CC as coronary bypass and organ transplantation surgery
 XX Sequence 14 AA;
 SQ

Query Match 100.0%; Score 83; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RRP 14
 |||||
 Db 1 RRRPRPPYLP RRP 14

RESULT 3

ADE86118
 ID ADE86118 standard; peptide; 14 AA.

XX
 AC ADE86118;

XX 29-JAN-2004 (first entry)

DE Proline-arginine (PR)-rich antimicrobial peptide PR-14.

XX Leukocyte superoxide anion; leukocyte O2- production;
 KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;
 KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;
 KW tissue damage; oxygen radical; antibacterial.

XX Synthetic.

XX US2003125249-A1.

XX 03-JUL-2003.

XX 07-DEC-2001; 2001US-00014147.

XX 10-APR-1995; 95US-00419066.

XX 08-OCT-1997; 97US-00930777.

XX (BLEC/) BLECHA F.

XX (SHIJ/) SHI J.

XX Blecha F, Shi J;

XX WPI; 2004-059188/06.

XX Attracting leukocyte to location by administering peptide including
 PT proline-arginine-rich antimicrobial peptide or its truncated analogs to
 PT the location.

XX Claim 3; SEQ ID NO 7; 24pp; English.

XX The present invention relates to a method of inhibiting leukocyte
 CC superoxide anion (O2-) production and/or attracting leukocytes. The
 CC method comprises the use of proline-arginine (PR)-rich antimicrobial
 CC peptides or their truncated analogues. The method is useful for
 CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or
 CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are
 CC useful as medicaments to fight infection by attracting leukocytes to a
 CC wound site, while restricting tissue damage at the wound site caused by
 CC excessive oxygen radicals produced by these leukocytes. The present
 CC sequence represents a PR-rich antimicrobial peptide.

XX Sequence 14 AA;

Query Match 100.0%; Score 83; DB 8; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RRP 14
 |||||
 Db 1 RRRPRPPYLP RRP 14

RESULT 4
ADL67260
ID ADL67260 standard; peptide; 14 AA.
XX
AC ADL67260;
XX
DT -20-MAY-2004 (first entry)
XX
DE Antimicrobial peptide PR-39 analog PR-14.
XX
KW Leucocyte; superoxide anion; oxygen radical; proline-arginine;
KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;
KW infection; wound; tissue damage; PR-39 analog; PR-14.
XX
OS Unidentified.
XX
PN US2004043934-A1.
XX
PD 04-MAR-2004.
XX
PF 28-AUG-2003; 2003US-00651147.
XX
PR 10-APR-1995; 95US-00419066.
PR 08-OCT-1997; 97US-00930777.
XX
PA (BLEC/) BLECHA F.
PA (SHIJ/) SHI J.
XX
PI Blecha F, Shi J;
XX
WPI; 2004-225728/21.
XX
XX Inhibiting leukocyte oxygen radical production comprises contacting a
PT leukocyte with a peptide, where the inhibition occurs as a consequence of
PT binding between the peptide and p47phox.
XX
PS Example; SEQ ID NO 7; 24pp; English.
XX
CC The invention relates to inhibiting leukocyte superoxide anion (O2-)
CC production using a naturally occurring proline-arginine (PR)-rich
CC antimicrobial peptide known as PR-39 and its truncated analogs. The
CC method comprises contacting leukocytes with the peptide comprising 39 or
CC 26 amino acids, for a time and under conditions effective to inhibit
CC leukocyte superoxide anion production. The peptide inhibits the activity
CC of NADPH oxidase responsible for anion production, by binding to Src
CC homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein
CC of the phagocytic NADPH oxidase complex. The leucocyte is a mammalian or
CC porcine leucocyte and the mammalian leucocyte is neutrophil. Another
CC method is also disclosed which employs a PR-39 analog that comprise 16
CC amino acids, where the sum of the proline and arginine residues in the
CC effective peptide is at least 66 or 74 % of the total number of amino
CC acids. This peptide inhibits leukocyte O2- production by the effective
CC binding to p47phox in whole cells, therefore interfering with the binding
CC of p47phox to p22phox. At least 14 or 25% of the amino acid residues in
CC the peptide are arginine residues. The method of the invention is useful
CC for inhibiting leukocyte oxygen radical production. The peptides are
CC useful as medicaments for fighting infections by attracting leucocytes to
CC a wound site, yet restrict tissue damage at the wound site caused by
CC excessive oxygen radicals produced by these leucocytes. The present
CC sequence is PR-39 analog, PR-14.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 83; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPRPPYLPRRP 14
DB 1 RRRPRPPYLPRRP 14

RESULT 5
AAB26885
ID AAB26885 standard; peptide; 15 AA.
XX
AC AAB26885;
XX
DT 01-FEB-2001 (first entry)
XX
DE PR-39 derived angiogenesis regulatory peptide 1.
XX
KW Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;
KW myocardial ischaemia; proteasome.
XX
OS Synthetic.
XX
PN WO200057895-A1.
XX
PD 05-OCT-2000.
XX
PF 16-MAR-2000; 2000WO-US007050.
XX
PR 26-MAR-1999; 99US-00276868.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Simons M, Gao Y;
XX
WPI; 2000-628319/60.
XX
XX Stimulating angiogenesis in situ, useful e.g. for treating anoxia and
PT infarction, by administering a PR-39 oligopeptide that regulates
PT enzymatic activity of proteasomes.
XX
PS Claim 12; Page 40; Sipp; English.
XX
CC This invention relates to a method for the stimulation of angiogenesis in
CC situ within a targeted collection of viable cells. The method comprises
CC introducing, into the cytoplasm, at least 1 member of the PR-39
CC oligopeptide collective, which interacts with cytoplasmic proteasomes.
CC Part of the proteolytic activity of the proteasomes is selectively
CC altered so as to stimulate angiogenesis. The method is used to induce
CC angiogenesis in tissue that has suffered anoxia or infarction, e.g.
CC myocardial infarction or chronic myocardial ischaemia, and also to study
CC the mechanisms that control angiogenesis. The present sequence represents
CC a PR-39 derived peptide which interacts with the proteasome and can be
CC used in the method of the invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14
DB 1 RRRPRPPYLPRRP 14

RESULT 6
AAB97277
ID AAB97277 standard; peptide; 15 AA.
XX
AC AAB97277;
XX
DT 09-AUG-2001 (first entry)
XX
DE PR-39 derived peptide PR-15.
XX

PR-39; cathelin; inflammation; wound healing; myocardial infarction;
KW proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;
KW anoxia; chronic myocardial ischaemia; heart tissue.
XX

OS Unidentified.
 PN WO200130368-A1.
 XX PD 03-MAY-2001.
 XX PF 06-OCT-2000; 2000WO-US027552.
 XX PR 25-OCT-1999; 99US-00426011.
 XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX PI Simons M, Gao Y;
 XX DR WPI; 2001-355179/37.
 XX PT Stimulation of angiogenesis and inhibition of proteasome mediated
 PT degradation in cells, by introduction of PR-39 oligopeptide or its N-
 PT terminal fragments or their conjugates, for use in anoxia and infarction
 PT conditions.
 XX PS Claim 12; Page 42; 52pp; English.
 XX CC Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39
 CC is a member of the cathelin family of proteins, mature PR-39 is 39
 CC amino acids in length (see AAB97280), and has been shown to play a role
 CC in several inflammatory events including wound healing and myocardial
 CC infarction. The PR-39 derived family of oligopeptides cause selective
 CC inhibition of proteasome mediated degeneration of peptides and
 CC stimulation of angiogenesis after their intracellular introduction to a
 CC target cell. PR-39 derived peptides are able to interact with at least
 CC the alpha7 subunit of the proteasomes, and therefore alter the
 CC proteolytic activity of proteasomes such that a selective increased
 CC expression of specific proteins occurs. The invention includes methods
 CC for the selective inhibition of proteasome mediated peptide degradation.
 CC The method provides means for stimulating angiogenesis as required in
 CC living tissues and organs which have suffered defects or have undergone
 CC anoxia and/or infarction, myocardial infarction or chronic myocardial
 CC ischaemia of heart tissue. Examples are the myocardium, skeletal or
 CC smooth muscle, artery or vein, lung, brain, kidney, spleen, liver,
 CC gastrointestinal or nerve tissues, limbs, and extremities. A particular
 CC example is after myocardial infarction or ischaemia
 XX Sequence 15 AA;
 SQ Query Match 100.0%; Score 83; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRRPRPPVLP RRP 14
 Db 1 RRRPRPPVLP RRP 14
 RESULT 7
 AAB84691
 ID AAB84691 standard; peptide; 15 AA.
 XX AC AAB84691;
 XX DT 17-SEP-2001 (first entry)
 XX DE Amino acid sequence of a PR-39 derived peptide (residues 1-15).
 XX PR-39; IkappaBalpha degradation; NFkappaB transcription factor;
 KW myocardial infarction; chronic myocardial ischemia; heart disease;
 KW anoxia.
 XX OS Unidentified.
 XX WO200147540-A1.
 XX PD 05-JUL-2001.

XX 27-DEC-2000; 2000WO-US035293.
 XX 29-DEC-1999; 99US-00474967.
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX PI Simons M, Gao Y;
 XX DR WPI; 2001-441690/47.
 XX PT Selective inhibition of IkappaBalpha degradation within targeted viable
 PT cell collection, involves interacting PR-39 oligopeptide with
 PT IkappaBalpha and proteasomes, and altering proteolytic activity of
 PT proteasomes.
 XX Claim 11; Page 58; 69pp; English.
 XX PS The present sequence represents a PR-39 derived peptide. It is used for
 CC selective inhibition of IkappaBalpha degradation within a targeted cell
 CC collection in-situ. The method is useful for selectively inhibiting
 CC IkappaBalpha protein degradation in situ, decreasing the activity of
 CC NFkappaB transcription factor and selective control of NFkappaB-dependent
 CC gene expression in situ. The PR-39 derived peptides are useful in the
 CC treatment of myocardial infarction, chronic myocardial ischemia of heart
 CC disease and anoxia
 XX Sequence 15 AA;
 SQ Query Match 100.0%; Score 83; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRRPRPPVLP RRP 14
 Db 1 RRRPRPPVLP RRP 14
 RESULT 8
 AAW01452
 ID AAW01452 standard; peptide; 19 AA.
 XX AC AAW01452;
 XX DT 18-JUN-1997 (first entry)
 XX DE Leukocyte O2- production inhibitor peptide PR19.
 XX KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
 KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 KW tissue damage; oxygen radical; inflammatory disease; therapy.
 XX OS Synthetic.
 XX WO9632129-A1.
 XX PD 17-OCT-1996.
 XX PF 10-APR-1996; 96WO-US004674.
 XX PR 10-APR-1995; 95US-00419066.
 XX (UNIV) UNIV KANSAS STATE RES FOUND.
 XX PI Blecha F, Shi J;
 XX DR WPI; 1996-476842/47.
 XX PT Inhibition of leukocyte superoxide anion prodn. and attraction of
 PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.
 XX

PS Disclosure; Page 27; 45pp; English.

XX AAW01447-W01454 represent fragments of the proline-arginine rich

CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first

CC isolated from porcine small intestine, and has also been identified in

CC human and porcine neutrophils. PR39 kills bacteria by interfering with

CC DNA and/or protein synthesis. PR39 also induces syndecan expression on

CC mesenchymal cells. Syndecans are important in wound repair, showing that

CC PR39 can be used in wound repair, as well as in antibacterial agents.

CC These sequences, and PR39, can be used in the method of the invention.

CC The method of the invention is for inhibiting leukocyte superoxide anion

CC (O2-) production. The method comprises administering to a leukocyte a

CC peptide (such as this sequence) capable of inhibiting leukocyte O2-

CC production. The peptides can be used as medicaments for fighting

CC infection by attracting leukocytes to a wound site and restricting tissue

CC damage at the wound site caused by excessive oxygen radicals produced by

CC these leukocytes. They can also be used to develop products for treating

CC inflammatory disease states

XX

SQ Sequence 19 AA;

Query Match 100.0%; Score 83; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 0.0016;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPVLP RRP 14

DB 1 RRRPRPPVLP RRP 14

|||||

RESULT 9

ADB86115

ID ADE86115 standard; peptide; 19 AA.

XX

AC ADE86115;

XX

XX 29-JAN-2004 (first entry)

DE

XX Proline-arginine (PR)-rich antimicrobial peptide PR-19.

XX

KW Leukocyte superoxide anion; leukocyte O2- production;

KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;

KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;

KW tissue damage; oxygen radical; antibacterial.

XX

OS Synthetic.

XX

XX US2003125249-A1.

XX

PD 03-JUL-2003.

XX

XX 07-DEC-2001; 2001US-00014147.

XX

PR 10-APR-1995; 95US-00419066.

PR 08-OCT-1997; 97US-00930777.

XX

XX (BLEC/) BLECHA F.

XX (SHIJ/) SHI J.

XX

XX Blecha F, Shi J;

XX

XX WPI; 2004-059188/06.

XX

XX Attracting leukocyte to location by administering peptide including

XX proline-arginine-rich antimicrobial peptide or its truncated analogs to

XX the location.

XX

XX Example; SEQ ID NO 4; 24pp; English.

PS

XX The present invention relates to a method of inhibiting leukocyte

CC superoxide anion (O2-) production and/or attracting leukocytes. The

CC method comprises the use of proline-arginine (PR)-rich antimicrobial

CC peptides or their truncated analogues. The method is useful for

CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or

CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are

CC useful as medicaments to fight infection by attracting leukocytes to a

CC wound site, while restricting tissue damage at the wound site caused by

CC excessive oxygen radicals produced by these leukocytes. The present

CC sequence represents a PR-rich antimicrobial peptide.

XX

SQ Sequence 19 AA;

Query Match 100.0%; Score 83; DB 8; Length 19;

Best Local Similarity 100.0%; Pred. No. 0.0016;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPVLP RRP 14

DB 1 RRRPRPPVLP RRP 14

|||||

RESULT 10

ADL67257

ID ADL67257 standard; peptide; 19 AA.

XX

AC ADL67257;

XX

XX 20-MAY-2004 (first entry)

DT

XX Antimicrobial peptide PR-39 analog PR-19.

DE

XX Leucocyte; superoxide anion; oxygen radical; proline-arginine;

KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;

KW infection; wound; tissue damage; PR-39 analog; PR-19.

XX

OS Unidentified.

XX

XX US2004043934-A1.

XX

XX 04-MAR-2004.

XX

XX 28-AUG-2003; 2003US-00651147.

XX

XX 10-APR-1995; 95US-00419066.

PR 08-OCT-1997; 97US-00930777.

XX

XX (BLEC/) BLECHA F.

XX (SHIJ/) SHI J.

XX

XX Blecha F, Shi J;

XX

XX WPI; 2004-225728/21.

XX

XX Inhibiting leukocyte oxygen radical production comprises contacting a

PT leukocyte with a peptide, where the inhibition occurs as a consequence of

PT binding between the peptide and p47phox.

XX

XX Example; SEQ ID NO 4; 24pp; English.

XX

XX The invention relates to inhibiting leukocyte superoxide anion (O2-)

CC production using a naturally occurring proline-arginine (PR)-rich

CC antimicrobial peptide known as PR-39 and its truncated analogs. The

CC method comprises contacting leukocytes with the peptide comprising 39 or

CC 26 amino acids, for a time and under conditions effective to inhibit

CC leukocyte superoxide anion production. The peptide inhibits the activity

CC of NADPH oxidase responsible for anion production, by binding to Src

CC homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein

CC of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or

CC porcine leukocyte and the mammalian leukocyte is neutrophil. Another

CC method is also disclosed which employs a PR-39 analog that comprise 16

CC amino acids, where the sum of the proline and arginine residues in the

CC effective peptide is at least 66 or 74 % of the total number of amino

CC acids. This peptide inhibits leukocyte O2- production by the effective

CC binding to p47phox in whole cells, therefore interfering with the binding

CC of p47phox to p22phox. At least 14 or 25% of the amino acid residues in

CC the peptide are arginine residues. The method of the invention is useful

CC for inhibiting leukocyte oxygen radical production. The peptides are
 CC useful as medicaments for fighting infections by attracting leucocytes to
 CC a wound site, yet restrict tissue damage at the wound site caused by
 CC excessive oxygen radicals produced by these leucocytes. The present
 CC sequence is PR-39 analog, PR-19.

SQ Sequence 19 AA;

Query Match 100.0%; Score 83; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPVLP RPRP 14
 |||||
 DB 1 RRRPRPPVLP RPRP 14

RESULT 11
 AAW01447
 ID AAW01447 standard; peptide; 26 AA.

AC AAW01447;

DT 18-JUN-1997 (first entry)

DE Leukocyte O2- production inhibitor peptide PR26.

XX Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
 KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 KW tissue damage; oxygen radical; inflammatory disease; therapy.

XX Synthetic.

OS WO9632129-A1.

PN 17-OCT-1996.

PD 10-APR-1996; 96WO-US004674.

PF 10-APR-1995; 95US-00419066.

PR (UNIV) UNIV KANSAS STATE RES FOUND.

PS Blecha F, Shi J;

XX WPI; 1996-476842/47.

DR Inhibition of leukocyte superoxide anion prodn. and attraction of
 PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.

XX Claim 3; Page 26; 45pp; English.

PS AAW01447-W01454 represent fragments of the proline-arginine rich
 CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
 CC isolated from porcine small intestine, and has also been identified in
 CC human and porcine neutrophils. PR39 kills bacteria by interfering with
 CC DNA and/or protein synthesis. PR39 also induces syndecan expression on
 CC mesenchymal cells. Syndecans are important in wound repair, showing that
 CC PR39 can be used in wound repair, as well as in antibacterial agents.
 CC These sequences, and PR39, can be used in the method of the invention.
 CC The method of the invention is for inhibiting leukocyte superoxide anion
 CC (O2-) production. The method comprises administering to a leukocyte a
 CC peptide (such as this sequence) capable of inhibiting leukocyte O2-
 CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting tissue
 CC damage at the wound site caused by excessive oxygen radicals produced by
 CC these leukocytes. They can also be used to develop products for treating
 CC inflammatory disease states

XX Sequence 26 AA;

Query Match 100.0%; Score 83; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPVLP RPRP 14
 |||||
 DB 1 RRRPRPPVLP RPRP 14

RESULT 12
 AAW75723
 ID AAW75723 standard; peptide; 26 AA.

XX AAW75723;

XX 19-NOV-1998 (first entry)

XX Proline/Arginine rich peptide PR-26.

XX Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;
 KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;
 KW coronary bypass; organ transplantation surgery.

XX Synthetic.

XX WO9835690-A1.

XX 20-AUG-1998.

XX 17-FEB-1998; 98WO-US003207.

XX 18-FEB-1997; 97US-00802306.

XX 16-FEB-1998; 98US-00024975.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Ross CR, Blecha F, Shi J;

XX WPI; 1998-495359/42.

XX Reduction of reperfusion injury in temporarily occluded blood vessels -
 PT by administration of a peptide which is rich in proline or arginine
 PT residues.

XX Claim 3; Page 14-15; 35pp; English.

XX Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
 CC administration into a mammal's bloodstream reduce reperfusion injury
 CC (production of reactive oxygen species, neutrophil adherence to
 CC endothelium, and extravasation of neutrophils). These peptides have two
 CC requirements: they contain the consensus sequence PXXP, where P is a
 CC proline residue and X is any amino acid residue, which has been found to
 CC inhibit superoxide production, and secondly they have arginine residues
 CC adjacent to these motifs, required for effective inhibition. It was
 CC established by structural and function analysis that a peptide should
 CC ideally contain 4 or 6 of these motifs, and that inhibitory activity is
 CC correlated with the increase of length of peptides. The effectiveness of
 CC these peptides was determined by investigating the production of the
 CC neutrophil superoxide anion, and also the inhibition of neutrophil
 CC chemotaxis. From this, it was found that all of the peptides inhibited
 CC NADPH oxidase to some extent. All of the peptides also inhibit neutrophil
 CC oxidase activity. PR-39 is believed, to be the most potent endogenous
 CC down regulator of NADPH oxidase yet discovered, and from the data
 CC produced, it can be suggested to be involved in eliminating or reducing
 CC the reperfusion injury induced adhesion and extraction of neutrophils.
 CC The peptides are also useful in connection with surgical procedures such
 CC as coronary bypass and organ transplantation surgery

XX Sequence 26 AA;

Query Match 100.0%; Score 83; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPLPRRP 14
Db 1 RRRPPPLPRRP 14

RESULT 13
ADE86113 standard; peptide; 26 AA.
AC ADE86113;
XX 29-JAN-2004 (first entry)
DT Proline-arginine (PR)-rich antimicrobial peptide PR-26.
DE Leukocyte superoxide anion; leukocyte O2- production;
KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;
KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;
KW tissue damage; oxygen radical; antibacterial.
XX Synthetic.
OS US2003125249-A1.
XX 03-JUL-2003.
XX 07-DEC-2001; 2001US-00014147.
XX 10-APR-1995; 95US-00419066.
XX 08-OCT-1997; 97US-00930777.
XX (BLEC/) BLECHA F.
XX (SHIJ/) SHI J.
XX Blecha F, Shi J;
XX WPI; 2004-059188/06.
XX Attracting leukocyte to location by administering peptide including
XX proline-arginine-rich antimicrobial peptide or its truncated analogs to
XX the location.
XX Claim 3; SEQ ID NO 2; 24pp; English.
XX The present invention relates to a method of inhibiting leukocyte
XX superoxide anion (O2-) production and/or attracting leukocytes. The
XX method comprises the use of proline-arginine (PR)-rich antimicrobial
XX peptides or their truncated analogues. The method is useful for
XX attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or
XX a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are
XX useful as medicaments to fight infection by attracting leukocytes to a
XX wound site, while restricting tissue damage at the wound site caused by
XX excessive oxygen radicals produced by these leukocytes. The present
XX sequence represents a PR-rich antimicrobial peptide.
XX Sequence 26 AA;
XX Query Match 100.0%; Score 83; DB 8; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 0.0021;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPLPRRP 14
Db 1 RRRPPPLPRRP 14

RESULT 14
ADL67255 standard; peptide; 26 AA.
XX ADL67255;
AC ADL67255;
XX

DT 20-MAY-2004 (first entry)
XX Antimicrobial peptide PR-39 analog PR-26.
XX Leukocyte; superoxide anion; oxygen radical; proline-arginine;
KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;
KW infection; wound; tissue damage; PR-39 analog; PR-26.
XX Unidentified.
XX Key Location/Qualifiers
XX FH 1..3
XX FT /note= "Essential for antibacterial activity"
XX FT 20..26
XX FT /note= "Essential for antibacterial activity"
XX US2004043934-A1.
XX 04-MAR-2004.
XX 28-AUG-2003; 2003US-00651147.
XX 10-APR-1995; 95US-00419066.
XX 08-OCT-1997; 97US-00930777.
XX (BLEC/) BLECHA F.
XX (SHIJ/) SHI J.
XX Blecha F, Shi J;
XX WPI; 2004-225728/21.
XX Inhibiting leukocyte oxygen radical production comprises contacting a
XX leukocyte with a peptide, where the inhibition occurs as a consequence of
XX binding between the peptide and p47phox.
XX Claim 1; SEQ ID NO 2; 24pp; English.
XX The invention relates to inhibiting leukocyte superoxide anion (O2-)
XX production using a naturally occurring proline-arginine (PR)-rich
XX antimicrobial peptide known as PR-39 and its truncated analogs. The
XX method comprises contacting leukocytes with the peptide comprising 39 or
XX 26 amino acids, for a time and under conditions effective to inhibit
XX leukocyte superoxide anion production. The peptide inhibits the activity
XX of NADPH oxidase responsible for anion production, by binding to Src
XX homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein
XX of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or
XX porcine leukocyte and the mammalian leukocyte is neutrophil. Another
XX method is also disclosed which employs a PR-39 analog that comprises 16
XX amino acids, where the sum of the proline and arginine residues in the
XX effective peptide is at least 66 or 74 % of the total number of amino
XX acids. This peptide inhibits leukocyte O2- production by the effective
XX binding to p47phox in whole cells, therefore interfering with the binding
XX of p47phox to p22phox. At least 14 or 25% of the amino acid residues in
XX the peptide are arginine residues. The method of the invention is useful
XX for inhibiting leukocyte oxygen radical production. The peptides are
XX useful as medicaments for fighting infections by attracting leukocytes to
XX a wound site, yet restrict tissue damage at the wound site caused by
XX excessive oxygen radicals produced by these leukocytes. The present
XX sequence is PR-39 analog PR-26.
XX Sequence 26 AA;
XX Query Match 100.0%; Score 83; DB 8; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 0.0021;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPLPRRP 14
Db 1 RRRPPPLPRRP 14

RESULT 15

```

AAR30491
ID  AAR30491 standard; peptide; 39 AA.
XX
XX  AC      AAR30491;
XX
XX  DT      25-MAR-2003 (revised)
XX  DT      12-MAY-1993 (first entry)
XX
XX  DE      Antibacterial peptide.
XX
XX  KW      Pig; small intestine; endocrine; gram negative; bacteria; therapeutic;
XX  KW      veterinary medicine; prophylactic.
XX
XX  OS      Sus scrofa domestica.
XX
XX  PN      WO9222578-A1.
XX
XX  PD      23-DEC-1992.
XX
XX  PF      10-JUN-1992; 92WO-SE000394.
XX
XX  PR      14-JUN-1991; 91SE-00001838.
XX
XX  PA      (LEEJ/) LEE J.
XX  PA      (BONA/) BOMAN H G.
XX  PA      (MUTT/) MUTT V.
XX  PA      (JOER/) JOERNVALL H.
XX
XX  PI      Lee J, Boman HG, Mutt V, Joernvall H;
XX
XX  DR      WPI; 1993-018080/02.
XX
XX  PT      New anti-bacterial polypeptide - active against Gram negative bacteria.
XX
XX  PS      Claim 1; Page 10; 15pp; English.
XX
XX  CC      This peptide was isolated from the small intestine of a pig. The small
XX  CC      intestine is an important endocrine organ and many physiologically active
XX  CC      peptides have been isolated from it. This peptide inhibits the growth of,
XX  CC      and may kill, bacteria, pref. gram negative bacteria. This peptide or its
XX  CC      functional derivatives may be used in human or veterinary medicine for
XX  CC      therapeutic or prophylactic use. (Updated on 25-MAR-2003 to correct PN
XX  CC      field.)
XX
XX  SQ      Sequence 39 AA;

Query Match      100.0%; Score 83; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPRPPYLPRPRP 14
      |||||
Db      1 RRRPRPPYLPRPRP 14

Search completed: October 26, 2005, 05:12:08
Job time : 55.1091 secs

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:00:14 ; Search time 10.4364 Seconds
(without alignments)
129.071 Million cell updates/sec

Title: US-10-014-147-7

Perfect score: 83

Sequence: 1 RRRPPPLPRRP 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	83	100.0	172	2 S68232	antimicrobial prot
2	66	79.5	59	2 A36589	bactenecin 7 - bov
3	58	69.9	190	2 S68230	antimicrobial pept
4	53	63.9	184	2 T29373	hypothetical prote
5	52.5	63.3	82	2 A41051	spore coat protein
6	52	62.7	1006	2 G86292	hypothetical prote
7	51.5	62.0	1187	1 JC4155	protein-tyrosine-p
8	51.5	62.0	1189	1 JC2366	hypothetical prote
9	50	60.2	192	2 S76867	apidaecin 14 precu
10	49.5	59.6	168	2 S35330	extensin class I
11	49.5	59.6	199	2 S14981	hypothetical prote
12	49	59.0	210	2 T33700	hypothetical prote
13	49	59.0	218	2 T22261	hypothetical prote
14	49	59.0	589	2 T29299	hypothetical prote
15	48	57.8	134	2 AC0665	probable cytochrom
16	48	57.8	139	2 S09612	hypothetical xrep8
17	48	57.8	261	1 WMBXE	infected cell prot
18	48	57.8	402	1 VGBE50	glycoprotein D pre
19	48	57.8	437	2 A88942	protein R13D11.3
20	48	57.8	520	2 T04591	ferulate-5-hydroxy
21	47.5	57.2	301	2 JQ1663	hybrid proline-ric
22	47	56.6	196	2 B48232	cysteine-rich exte
23	47	56.6	209	2 A48232	cysteine-rich exte
24	47	56.6	258	2 SS0336	tyrosine-rich hydr
25	47	56.6	359	2 T13478	hypothetical prote
26	47	56.6	427	2 T32652	hypothetical prote
27	47	56.6	456	2 T35474	50kD proline rich
28	47	56.6	665	2 D96621	auxin response fac
29	47	56.6	693	2 JN0673	ubiquitin-like fus

ALIGNMENTS

RESULT 1

S68232

antimicrobial protein PR-39 precursor, cathelin-associated - pig

N/Alternate names: myeloid antibacterial protein PR-39

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S68232; JN0899; I47138; S19563

R/Zhao, C.; Ganz, T.; Lehrer, R.I.

FEBS Lett. 376, 130-134, 1995

A/Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni

A/Reference number: S68232; MUID:96105365; PMID:7498526

A/Accession: S68232

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-172 <ZHA>

A/Cross-references: UNIPROT:P80054; EMBL:X89201; NID:g1165150; PIDN:CAA61487.1; PID:g116:

A/Experimental source: leukocytes

R/Storici, P.; Zanetti, M.

Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993

A/Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the i

A/Reference number: JN0899; MUID:94071853; PMID:8250863

A/Accession: JN0899

A/Molecule type: mRNA

A/Residues: 1-20, 'A', 22-172 <STO>

A/Cross-references: GB:L23825; NID:g435100; PIDN:AAA31109.1; PID:g435101

A/Experimental source: bone marrow cells

R/Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bone

Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995

A/Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fami

A/Reference number: I47138; MUID:95350216; PMID:7624374

A/Accession: I47138

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-28, 'T', 30-89, 'QR', 92-116, 'NDP', 120-172 <GUD>

A/Cross-references: EMBL:X87236; NID:g829142; PIDN:CAA60682.1; PID:g1051298

R/Aggerberth, B.; Les, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall,

Eur. J. Biochem. 202, 849-854, 1991

A/Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of t

A/Reference number: S19563; MUID:92111534; PMID:1765098

A/Accession: S19563

A/Molecule type: protein

A/Residues: 131-169 <AGE>

A/Experimental source: intestine

C/Genetics:

A/Gene: PR39

A/Introns: 66/3; 102/3; 126/3

C/Superfamily: cathelin; cystatin homology

C/Keywords: amidated carboxyl end; antibacterial

F/1-29/Domain: signal sequence #status predicted <SIG>

F/22-129/Domain: cystatin homology <CYS>

F/30-130/Domain: propeptide #status predicted <PRO>

F/131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>

hypothetical protein ZC404.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T29373

C;Comment: This structural protein is expressed during stage V of sporulation.

C;Genetics:

A;Gene: cotT

A;Start codon: TTG

C;Keywords: sporulation

F;1-19/Domain: propeptide #status experimental <PRO>

F;20-82/Product: spore coat protein #status experimental <WAT>

Query Match 63.3%; Score 52.5; DB 2; Length 82;
Best Local Similarity 83.3%; Pred. No. 2.3;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 4 PRPPYLPRLPRP 14

|||||

DB 49 PRPPYYPRPRP 60

RESULT 6

G86292

hypothetical protein F7H2.17 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: G86292

R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: G86292

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1006 <STO>

A;Cross-references: UNIPROT:Q9LMQ1; GB:AE005172; NID:g8927662; PIDN:AAF82153.1; GSPDB:GN

C;Genetics:

A;Map position: 1

Query Match 62.7%; Score 52; DB 2; Length 1006;

Best Local Similarity 81.8%; Pred. No. 31;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PRPPYLPRLPRP 14

|||||

DB 99 PRPPRPRPRP 109

RESULT 7

JC4155

protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - human

N;Alternate names: PEZ protein; protein-tyrosine-phosphatase/ezrin-like protein

C;Species: Homo sapiens (man)

C;Date: 27-Aug-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C;Accession: JC4155

R;Smith, A.L.; Mitchell, P.J.; Shipley, J.; Gusterson, B.A.; Rogers, M.V.; Crompton, M.R.

Biochem. Biophys. Res. Commun. 209, 959-965, 1995

A;Title: PEZ: a novel human cDNA encoding protein tyrosine phosphatase and ezrin-like dom

A;Reference number: JC4155; MUID:95251727; PMID:7733990

A;Accession: JC4155

A;Molecule type: mRNA

A;Residues: 1-1187 <SMI>

A;Cross-references: UNIPROT:Q15678; EMBL:X82676; NID:g3929753; PIDN:CAA57993.1; PID:g809

A;Experimental source: Breat

C;Genetics:

A;Gene: GDB:PTPN14

A;Cross-references: GDB:454485

A;Map position: 1q32.2-1q32.2

C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b

C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatad

F;23-302/Domain: protein 4.1 membrane-binding domain homology <B41>

F;566-575/Region: proline-rich

F;709-716/Region: acidic

F;933-1169/Domain: protein-tyrosine-phosphatase homology <PTP2>

F;1121/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1127/Binding site: substrate phosphate (Arg) #status predicted

Query Match 62.0%; Score 51.5; DB 1; Length 1187;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3 RRPYPYLPRLPRP 14

|||||

DB 565 RPPPPY-PRPRP 575

RESULT 8

JC2366

protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - mouse

N;Alternate names: PEZ protein; protein-tyrosine-phosphatase PTP36; protein-tyrosine-phos

C;Species: Mus musculus (house mouse)

C;Date: 24-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C;Accession: JC2366

R;Sawada, M.; Ogata, M.; Fujino, Y.; Hamaoka, T.

Biochem. Biophys. Res. Commun. 203, 479-484, 1994

A;Title: cDNA cloning of a novel protein tyrosine phosphatase with homology to cytoskelet

A;Reference number: JC2366; MUID:94354845; PMID:8074693

A;Accession: JC2366

A;Molecule type: mRNA

A;Residues: 1-1189 <SAM>

A;Cross-references: UNIPROT:Q62130; GB:D31842; NID:G507330; PIDN:BAA06628.1; PID:G507331

A;Experimental source: thymus

C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-bj

C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F;23-302/Domain: protein 4.1 membrane-binding domain homology <B41>

F;566-575/Region: proline-rich

F;712-718/Region: acidic

F;935-1171/Domain: protein-tyrosine-phosphatase homology <PTP2>

F;1123/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1129/Binding site: substrate phosphate (Arg) #status predicted

Query Match 62.0%; Score 51.5; DB 1; Length 1189;

Best Local Similarity 83.3%; Pred. No. 42;

Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3 RRPYPYLPRLPRP 14

|||||

DB 565 RPPPPY-PRPRP 575

RESULT 9

S76867

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S76867

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

S;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S76867

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-192 <KAN>

A;Cross-references: UNIPROT:P74661; EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA1877;

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 60.2%; Score 50; DB 2; Length 192;

Best Local Similarity 69.2%; Pred. No. 11;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 RRPYPYLPYLPYLP 14
 |||||
 Db 3 RRPYPYLPYLPYLP 15

RESULT 10

S3530
 apidaecin 14 precursor - honeybee
 N:Contains: apidaecin II
 C:Species: Apis mellifera (honeybee)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C:Accession: S35330; S06676
 R:Casteels-Josson, K.; Capaci, T.; Casteels, P.; Tempst, P.
 EMO J. 12, 1569-1578, 1993
 A:Title: Apidaecin multipetide precursor structure: a putative mechanism for amplification
 A:Reference number: S35330; MUID:93223697; PMID:8467807
 A:Accession: S35330
 A:Molecule type: mRNA
 A:Residues: 1-168 <CAS>
 A:Cross-references: UNIPROT:Q06601; EMBL:X72575; NID:g297062; PIDN:CAA51167.1; PID:g297062
 R:Casteels, P.; Ampe, C.; Jacobs, F.; Vaeck, M.; Tempst, P.
 EMO J. 8, 2387-2391, 1989
 A:Title: Apidaecins: antibacterial peptides from honeybees.
 A:Reference number: S05383; MUID:90005446; PMID:2676519
 A:Accession: S06676
 A:Molecule type: protein
 A:Residues: 43-60 <CA2>
 C:Superfamily: procylic acid repetitive protein
 F:43-60/Product: apidaecin II #status experimental <MAT>

Query Match 59.6%; Score 49.5; DB 2; Length 168;
 Best Local Similarity 47.6%; Pred. No. 11;
 Matches 10; Conservative 2; Mismatches 2; Indels 7; Gaps 1;

QY 1 RRPYPYLPYLPYLP 14
 |||||
 Db 117 RRPYPYLPYLPYLP 137

RESULT 11

S14981
 extensin class I (clone wi-8 L) - tomato (fragment)
 C:Species: Lycopersicon esculentum (tomato)
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 11-Jan-2000
 C:Accession: S14981
 R:Shawalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
 Plant Mol. Biol. 16, 547-565, 1991
 A:Title: Tomato extensin and extensin-like cDNAs: structure and expression in response to wounding
 A:Reference number: S14970; MUID:91329690; PMID:1714316
 A:Accession: S14981
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-199 <SHO>
 A:Cross-references: EMBL:X55692
 A:Experimental source: cv. UC82B
 C:Superfamily: hydroxyproline-rich glycoprotein
 C:Keywords: cell wall; glycoprotein; hydroxyproline

Query Match 59.6%; Score 49.5; DB 2; Length 199;
 Best Local Similarity 71.4%; Pred. No. 13;
 Matches 10; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 4 RRPYPYLPYLPYLP 14
 |||||
 Db 77 RRPYPYLPYLPYLP 90

RESULT 12

T33700
 hypothetical protein F49F1.9 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T33700
 R:Miller, N.; Wamsley, P.
 submitted to the EMBL Data Library, October 1998
 A:Description: The sequence of C. elegans cosmid F49F1.
 A:Reference number: Z21389
 A:Accession: T33700
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-210 <MIL>
 A:Cross-references: UNIPROT:Q9GZE0; EMBL:AF100656; PIDN:AAC68952.1; GSPDB:GN00022; CESP:F49F1
 A:Experimental source: strain Bristol N2; clone F49F1
 C:Genetics:
 A:Gene: CESP:F49F1.9
 A:Map position: 4
 A:Introns: 130/3

Query Match 59.0%; Score 49; DB 2; Length 210;
 Best Local Similarity 69.2%; Pred. No. 16;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 RRPYPYLPYLPYLP 14
 |||||
 Db 53 RRPYPYLPYLPYLP 65

RESULT 13

T22261
 hypothetical protein F46A8.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T22261
 R:Harris, B.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19539
 A:Accession: T22261
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-218 <WIL>
 A:Cross-references: UNIPROT:O01331; EMBL:Z81539; PIDN:CAB04391.1; GSPDB:GN00019; CESP:F46A8
 A:Experimental source: clone F46A8
 C:Genetics:
 A:Gene: CESP:F46A8.5
 A:Map position: 1
 A:Introns: 138/3

Query Match 59.0%; Score 49; DB 2; Length 218;
 Best Local Similarity 69.2%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 RRPYPYLPYLPYLP 14
 |||||
 Db 61 RRPYPYLPYLPYLP 73

RESULT 14

T29299
 hypothetical protein C50F7.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T29299
 R:Johnson, D.; Stellyses, L.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C50F7.
 A:Reference number: Z20601
 A:Accession: T29299
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-589 <JOH>
 A:Cross-references: UNIPROT:Q18756; EMBL:U41557; PIDN:AAA83307.1; CESP:C50F7.2
 C:Genetics:
 A:Gene: CESP:C50F7.2
 A:Introns: 12/2
 C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology

Query Match 59.0%; Score 49; DB 2; Length 218;
 Best Local Similarity 69.2%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 RRPYPYLPYLPYLP 14
 |||||
 Db 61 RRPYPYLPYLPYLP 73

Query Match 59.0%; Score 49; DB 2; Length 589;
Best Local Similarity 81.8%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RRPRLPRP 12
| | | | |
Db 105 RRPRLPRP 115

RESULT 15

AC0665
probable cytochrome STY1431 [imported] - Salmonella enterica subsp. enterica serovar Typh
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0665
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AC0665
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-134 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD01692.1; PID:gl6502543; GSPDB:GN00176
C:Genetics:
A:Gene: STY1431

Query Match 57.8%; Score 48; DB 2; Length 134;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PRPRLPRP 14
| | | | |
Db 25 FTPIVPRPKP 35

Search completed: October 26, 2005, 05:20:02
Job time : 11.4364 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:52:03 ; Search time 48,4909 Seconds
(without alignments)
147.844 Million cell updates/sec

Title: US-10-014-147-7
Perfect score: 83
Sequence: 1 RRRPRPPYLP RRP 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	172	1 PR39_PIG	P80054 sus scrofa
2	66	79.5	190	1 BCT7_BOVIN	P19661 bos taurus
3	59	71.1	166	2 Q6VY72	Q6VY72 bacteriophage
4	58	69.9	164	2 P79361	P79361 ovis aries
5	58	69.9	190	1 BCT7_SHEEP	P50415 ovis aries
6	58	69.9	190	2 Q9X5G9	Q9X5G9 capra hircu
7	58	69.9	224	2 Q19031	Q19031 ovis aries
8	57	68.7	200	2 Q9RK54	Q9RK54 streptomyce
9	57	68.7	361	2 Q9XCG4	Q9XCG4 mycobacteri
10	55	66.3	337	2 Q7F1E7	Q7F1E7 oryza sativ
11	54	65.1	336	2 Q68405	Q68405 human cytom
12	53.5	64.5	397	2 Q7XTY0	Q7XTY0 oryza sativ
13	53	63.9	184	2 Q23291	Q23291 caenorhabdi
14	53	63.9	273	2 Q82P26	Q82P26 streptomyce
15	53	63.9	381	1 PRLP_BOVIN	Q9GKNS bos taurus
16	52.5	63.3	82	1 COTT_BACSU	P11863 bacillus su
17	52	62.7	421	2 Q84R66	Q84R66 oryza sativ
18	52	62.7	1006	2 Q9LMQ1	Q9LMQ1 arabidopsis
19	51.5	62.0	159	2 Q856G1	Q856G1 oryza sativ
20	51.5	62.0	472	2 Q8C3A1	Q8C3A1 mus musculu
21	51.5	62.0	876	2 Q8CEB8	Q8CEB8 mus musculu
22	51.5	62.0	957	2 Q8CAV9	Q8CAV9 mus musculu
23	51.5	62.0	1187	1 PTNE_HUMAN	Q15678 homo sapien
24	51.5	62.0	1189	1 PTNE_MOUSE	Q62130 mus musculu
25	51	61.4	156	2 Q8RV32	Q8RV32 oryza sativ
26	51	61.4	194	2 Q6Z0W1	Q6Z0W1 oryza sativ
27	51	61.4	393	2 Q7QAH2	Q7QAH2 anopheles g
28	51	61.4	1729	2 Q8LLZ0	Q8LLZ0 oryza sativ
29	51	61.4	1729	2 Q7XGP6	Q7XGP6 oryza sativ
30	50.5	60.8	183	2 Q94J98	Q94J98 oryza sativ
31	50.5	60.8	432	2 Q96HM7	Q96HM7 homo sapien

32	50.5	60.8	1095	1 AT17_HUMAN	Q8te56 homo sapien
33	50	60.2	144	2 Q8LW3	Q8lnw3 oryza sativ
34	50	60.2	192	2 P74661	P74661 synechocyst
35	50	60.2	206	2 Q8PHZ0	Q8phz0 xanthomonas
36	50	60.2	344	2 Q69260	Q69260 bovine herp
37	50	60.2	380	2 Q72727	Q72727 homo sapien
38	50	60.2	384	2 Q6JAF9	Q6jaf9 sorghum bic
39	49.5	59.6	168	1 APL4_APIME	Q6jaf9 sorghum bic
40	49.5	59.6	177	2 Q9FSP4	Q06601 apis mellif
41	49.5	59.6	451	2 Q6SQM6	Q9fesp4 oryza sativ
42	49.5	59.6	602	2 Q66852	Q6eqw6 oryza sativ
43	49	59.0	195	2 Q9G6V2	Q66852 avian adeno
44	49	59.0	210	2 Q9GZE0	Q9g9v2 homo sapien
45	49	59.0	212	2 Q08306	Q9g9v2 caenorhabdi
					Q08306 nocardioid

ALIGNMENTS

RESULT 1

PR39_PIG STANDARD; PRT; 172 AA.
ID PR39_PIG STANDARD; PRT; 172 AA.
AC P80054; Q9TR84;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antibacterial protein PR-39 precursor.
GN Name=PR39;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=95350216; PubMed=7624374;
RX Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,
RA Andersson L., Boman H.G.;
RT "Structure of the gene for porcine peptide antibiotic PR-39, a
cathelin gene family member; comparative mapping of the locus for the
human peptide antibiotic FALL-39.";
RT Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089 (1995).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Bone marrow;
RC MEDLINE=94071853; PubMed=8250863;
RX Storici P., Zanetti M.;
RA "A cDNA derived from pig bone marrow cells predicts a sequence
RT identical to the intestinal antibacterial peptide PR-39.";
RL Biochem. Biophys. Res. Commun. 196:1058-1065 (1993).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;
RX Zhao C., Ganz T., Lehrer R.I.;
RA "Structures of genes for two cathelin-associated antimicrobial
RT peptides: prophenin-2 and PR-39.";
RL FEBS Lett. 376:130-134 (1995).
RN [4]
RN SEQUENCE OF 131-169.
RP TISSUE=Intestine;
RC MEDLINE=92111534; PubMed=1765098;
RX Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
RA Mutt V., Joernvall H.;
RT "Amino acid sequence of PR-39. Isolation from pig intestine of a new
RT member of the family of proline-arginine-rich antibacterial
peptides.";
RL Eur. J. Biochem. 202:849-854 (1991).
RN [5]
RN SEQUENCE OF 131-164, AND FUNCTION.
RP TISSUE=Neutrophils;
RC MEDLINE=95088504; PubMed=7996056;
RX Shi J., Ross C.R., Chengappa M.M., Blecha F.;
RT "Identification of a proline-arginine-rich antibacterial peptide from


```

7.5 kDa bactinecin (Fragment).
GN Name=Bac7.5; (Sheep).
OC Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP
RC SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96140591; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3;
RA Mahoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Huttner K.M.;
RT "Molecular analysis of the sheep cathelin family reveals a novel
RT antimicrobial peptide.";
RT FEBS Lett. 377:519-522(1995).
RN [2]
RP
RC SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Huttner K.M., Mahoney M.M.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR ENBL; U60598; AAB49713.1; -.
DR HSSP; P32196; 1KWI.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001894; Cathelcidin.
DR Pfam; PF00666; Cathelcidins; 1.
DR PRODOM; PD001838; Cathelcidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
FT NON TER 164 164
SQ SEQUENCE 164 AA; 18642 MW; E3BFC871F6AE8B9A CRC64;

Query Match 69.9%; Score 58; DB 2; Length 164;
Best Local Similarity 78.6%; Pred. NO. 5.3;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 RRRPRPPYLRPRP 14
| | | | |
Db 132 RLRPRRPLRPRP 145

RESULT 5
BC17_SHEEP STANDARD; PRT; 190 AA.
AC PS0415;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bactenechin 7 precursor (BAC7).
GN Name=BAC7.5;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP
RC SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96105386; PubMed=7498547; DOI=10.1016/0014-5793(95)01285-3;
RA Bagella L., Scoocchi M., Zanetti M.;
RT "cDNA sequences of three sheep myeloid cathelcidins.";
RT FEBS Lett. 376:225-228(1995).
CC -!- FUNCTION: Exerts, in vitro, a potent antimicrobial activity.
CC Probably due to an impairment of the function of the respiratory
CC chain and of energy-dependent activities in the inner membrane of
CC susceptible microorganisms (By similarity).
CC -!- SIMILARITY: Belongs to the cathelcidin family.
-----
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 DR EMBL; L46852; AAA85468.1; -;
 DR PIR; S68230; S68230.
 DR HSSP; P32196; 1KWI.
 DR InterPro; IP0001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidin; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 KW Antibiotic; Pyrrolidone carboxylic acid; Repeat; Signal.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 130 By similarity.
 FT CHAIN 131 190 Bactenecin 7.
 FT MOD_RES 30 30 Pyrrolidone carboxylic acid (By
 similarity)
 FT DISULFID 85 96 By similarity.
 FT DISULFID 107 124 By similarity.
 SQ SEQUENCE 190 AA; 21829 MW; E4AFAFBL600E98371 CRC64;
 Query Match 69.9%; Score 58; DB 1; Length 190;
 Best Local Similarity 78.6%; Pred. No. 6.2;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPVLP RRP 14
 | | | | |
 Db 132 RLRRPRRLPRRP 145

RESULT 6

Q9XSQ9 PRELIMINARY; PRT; 190 AA.
 AC Q9XSQ9;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Bac7.5 protein.
 GN Name=bac7.5;
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Zhao C., Nguyen T., Brogden K., Lehrer R.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ243125; CAB45523.1; -;
 DR HSSP; P32196; 1KWI.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0004952; P:defense response; IEA.
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
 DR InterPro; IP0001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR PROSITE; PD001838; Cathelicidin; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 FT CHAIN 131 190 Bac7.5 protein.
 SQ SEQUENCE 190 AA; 21835 MW; D1305EF16875F4F CRC64;

Query Match 69.9%; Score 58; DB 2; Length 190;
 Best Local Similarity 78.6%; Pred. No. 6.2;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPVLP RRP 14
 | | | | |
 Db 132 RLRRPRRLPRRP 145

RESULT 7

Q9XSQ9 PRELIMINARY; PRT; 200 AA.

Ol9031
 ID Ol9031 PRELIMINARY; PRT; 224 AA.
 AC Ol9031;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Bactinecin 11.
 GN Name=Bac11;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huttner K.M., Mahoney M.M.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U77049; AAB62000.1; -;
 DR EMBL; U77046; AAB62000.1; JOINED.
 DR EMBL; U77047; AAB62000.1; JOINED.
 DR EMBL; U77048; AAB62000.1; JOINED.
 DR HSSP; P32196; 1KWI.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
 DR InterPro; IP0001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidin; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 SQ SEQUENCE 224 AA; 25669 MW; 6AEAAAB1256AC76FC CRC64;

Query Match 69.9%; Score 58; DB 2; Length 224;
 Best Local Similarity 78.6%; Pred. No. 7.4;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPVLP RRP 14
 | | | | |
 Db 132 RLRRPRRLPRRP 145

RESULT 8

Q9RK54 PRELIMINARY; PRT; 200 AA.
 ID Q9RK54;
 AC Q9RK54;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein SCO0323.
 GN ORFNames=SCF12.02c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAINS=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL939105; CAB56128.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 200 AA; 22076 MW; 0DCBEC5585803B5 CRC64;

Query Match 68.7%; Score 57; DB 2; Length 200;
 Best Local Similarity 76.9%; Pred. No. 8.8;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRRP 13
 |||||
 DB 118 RRRPPPYLPRRP 130

RESULT 9

O9XCG4 PRELIMINARY; PRT; 361 AA.
 AC O9XCG4 (TREMELrel. 12, Created)
 DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Mycobacterium avium.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1764;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2151.
 RX MEDLINE=22885473; PubMed=14523113; DOI=10.1099/mic.0.26528-0;
 RA Eckstein T.M., Belisle J.T., Inamine J.M.;
 RT "Proposed pathway for the biosynthesis of serovar-specific
 RT glycopeptidolipids in Mycobacterium avium serovar 2";
 RL Microbiology 149:2797-2807(2003).
 DR EMBL; AF143772; RAD44199.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 361 AA; 40208 MW; AD01DBE825C1C9EA CRC64;

Query Match 68.7%; Score 57; DB 2; Length 361;
 Best Local Similarity 71.4%; Pred. No. 16;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRRP 14
 |||||
 DB 32 RRRPPPYLPRRP 45

RESULT 10

O7F1E7 PRELIMINARY; PRT; 337 AA.
 AC O7F1E7 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Putative amino acid permease.
 GN Name=OJ1191.A10.117;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003888; BAD11568.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
 DR GO; GO:0006865; P:amino acid transport; IEA.
 DR InterPro; IPR002293; A/rel_permease.
 KW Transmembrane.
 SQ SEQUENCE 337 AA; 36544 MW; 4053C3635F9CF6CC CRC64;

Query Match 66.3%; Score 55; DB 2; Length 337;
 Best Local Similarity 76.9%; Pred. No. 27;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRRPPPYLPRRP 14
 |||||
 DB 320 RRRPPPYLPRRP 332

RESULT 11

O68405 PRELIMINARY; PRT; 336 AA.
 AC O68405 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Orf UL151.
 OS Human cytomegalovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=10359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Toledo;
 RX MEDLINE=96099416; PubMed=8523595;
 RA Cha T.A., Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;
 RT "Human cytomegalovirus clinical isolates carry at least 19 genes not
 RT found in laboratory strains";
 RL J. Virol. 70:78-83(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Toledo;
 RX Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RL EMBL; U3331; AAA85892.1; -;
 DR EMBL; U3331; AAA85892.1; -;
 SQ SEQUENCE 336 AA; 35116 MW; 9F865E5019F69DOC CRC64;

Query Match 65.1%; Score 54; DB 2; Length 336;
 Best Local Similarity 76.9%; Pred. No. 36;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRRPPPYLPRRP 14
 |||||
 DB 279 RRRPPPYLPRRP 291

RESULT 12

O7XTY0 PRELIMINARY; PRT; 397 AA.
 AC O7XTY0 (TREMELrel. 25, Created)
 DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE OSTJNa0019K04.17 protein.
 GN Name=OSTJNa0019K04.17;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=12447439; DOI=10.1038/nature01183;
 RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
 RA Liu X., Lu T. Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y., Zhang W.,
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 RA Han B.;
 RT "Sequence and analysis of rice chromosome 4";
 RL Nature 420:316-320(2002).
 DR EMBL; AL606640; CAD41670.3; -;
 DR Gramene; Q7XTY0; -;

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SQ SEQUENCE 397 AA; 43737 MW; BAFCS45CBA4B22 CRC64;
Query Match 64.5%; Score 53.5; DB 2; Length 397;
Best Local Similarity 84.6%; Pred. No. 50;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 RRRPPPYLPRRP 14
| ||||| |||||
DB 24 RRRPP-LPRRP 35

RESULT 13
ID Q23291 PRELIMINARY; PRT; 184 AA.
AC Q23291;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein ZC404.1.
GN Name=ZC404.1; ORFNames=ZC404.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology, the C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Bentley D., Le T.T.;
RT "The sequence of C. elegans cosmid ZC404.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U55363; AAA97967.1; -.
DR FIr; T29373; T29373.
DR WormBase; WBGene0022601; ZC404.1.
DR WormPep; ZC404.1; CE07592.
KW Hypothetical protein.
SQ SEQUENCE 184 AA; 21649 MW; 6D64D09EA91308F9 CRC64;

Query Match 63.9%; Score 53; DB 2; Length 184;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RRRPPPYLPRRP 12
| ||||| |||||
DB 26 RPRKPYLPRP 35

RESULT 14
Q82PZ6 PRELIMINARY; PRT; 273 AA.
ID Q82PZ6;
AC Q82PZ6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=SAV725;

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OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005023; BAC68435.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 273 AA; 29246 MW; FE024904356085C1 CRC64;

Query Match 63.9%; Score 53; DB 2; Length 273;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRRP 14
| ||||| | ||
DB 224 RRRPPPPARPGSRP 237

RESULT 15
PRLP_BOVIN
ID PRLP_BOVIN STANDARD; PRT; 381 AA.
AC Q9GKN8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Prolargin precursor (proline-arginine-rich end leucine-rich repeat
protein).
GN Name=PRELP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular cartilage;
RX MEDLINE=20576219; PubMed=11007795; DOI=10.1074/jbc.M007917200;
RA Bengtsson E., Asberg A., Heinegaard D., Sommerin Y., Spillmann D.;
RT "The amino-terminal part of PRELP binds to heparin and heparan
sulfate.";
RL J. Biol. Chem. 275:40695-40702(2000).
RN [2]
RP FUNCTION.
RX MEDLINE=21964083; PubMed=11847210; DOI=10.1074/jbc.M108285200;
RA Bengtsson E., Moergelin M., Sasaki T., Timpl R., Heinegaard D.,
RA Asberg A.;
RT "The leucine-rich repeat protein PRELP binds perlecan and collagens
and may function as a basement membrane anchor.";
RL J. Biol. Chem. 277:15061-15068(2002).
CC -!- FUNCTION: May anchor basement membranes to the underlying
connective tissue.
CC -!- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan
perlecan and triple helical collagens type I and type II.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.

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CC -!- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and
CC heparan sulfate. Binds collagens type I and type II through its
CC leucine-rich repeat domain.
CC -!- SIMILARITY: Belongs to the small leucine-rich proteoglycan (SLRP)
CC family. Class II subfamily.
CC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
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CC -----
CC EMBL; AF163568; AAC23723.1; -;
CC HSPSP; P25146; I06S.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000372; LRR_Nterm.
CC InterPro; IPR003591; LRR_Typ.
CC Pfam; PF00560; LRR; 11.
CC Pfam; PF01462; LRRNT; 1.
CC PRINTS; PR00019; LEURICHRPT.
CC SMART; SM00013; LRRNT; 1.
CC Extracellular matrix; Glycoprotein; Leucine-rich repeat; Repeat;
KW Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 381 Prolargin.
FT DOMAIN 72 88 Cys-rich.
FT REPEAT 94 113 LRR-S 1.
FT REPEAT 114 137 LRR-T 1.
FT REPEAT 138 161 LRR-T 2.
FT REPEAT 162 182 LRR-S 2.
FT REPEAT 183 206 LRR-T 3.
FT REPEAT 207 232 LRR-T 4.
FT REPEAT 233 253 LRR-S 3.
FT REPEAT 254 277 LRR-T 5.
FT REPEAT 278 302 LRR-T 6.
FT REPEAT 303 322 LRR-S 4.
FT REPEAT 323 361 LRR-T 7.
FT REPEAT 362 381 LRR-T 8.
FT DOMAIN 196 201 Poly-Leu.
FT DISULFID 331 372 By similarity.
FT CARBOHYD 123 123 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 288 288 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 319 319 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 326 326 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 381 AA; 43682 MW; 23DA99C01BB772A0 CRC64;

Query Match 63.9%; Score 53; DB 1; Length 381;
Best Local Similarity 76.9%; Pred.No. 55;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RRRPPYLPRLRP 14
| | | | |
Db 25 RRRPRPRPRRP 37

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:02:04 ; Search time 14.3818 Seconds
(without alignments)
72.667 Million cell updates/sec

Title: US-10-014-147-7

Perfect score: 83
Sequence: 1 RRRPRPPLPRRP 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCUTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	14	3	US-09-024-975-4
2	83	100.0	14	4	US-08-930-777A-7
3	83	100.0	19	4	US-08-930-777A-4
4	83	100.0	26	2	US-08-419-066-2
5	83	100.0	26	3	US-09-024-975-2
6	83	100.0	26	4	US-08-930-777A-2
7	83	100.0	38	4	US-09-739-535-1
8	83	100.0	39	1	US-08-162-052-1
9	83	100.0	39	1	US-08-310-722-1
10	83	100.0	39	2	US-08-419-066-1
11	83	100.0	39	2	US-08-728-333-1
12	83	100.0	39	3	US-09-024-975-1
13	83	100.0	39	4	US-08-930-777A-1
14	83	100.0	39	5	PCT-US95-12080-1
15	68	81.9	23	4	US-08-930-777A-3
16	66	79.5	20	3	US-09-024-975-9
17	66	79.5	59	4	US-09-030-619-163
18	59	71.1	59	5	PCT-US95-12080-3
19	54	65.1	336	1	US-08-414-926A-26
20	54	65.1	336	2	US-08-926-822-26
21	54	65.1	336	3	US-09-253-682-26
22	54	65.1	336	3	US-09-527-657-26
23	54	65.1	336	4	US-09-892-100-26
24	54	65.1	594	4	US-09-252-991A-32578
25	51.5	62.0	381	4	US-09-252-991A-29050
26	51	61.4	159	4	US-09-252-991A-21389
27	51	61.4	642	4	US-09-252-991A-24767

28	51	61.4	955	4	US-09-252-991A-24254	Sequence 24254, A
29	50	60.2	193	4	US-09-252-991A-29164	Sequence 29164, A
30	50	60.2	879	4	US-09-252-991A-19784	Sequence 19784, A
31	49	59.0	26	3	US-09-024-975-8	Sequence 8, Appl
32	49	59.0	138	4	US-09-252-991A-32675	Sequence 32675, A
33	49	59.0	179	4	US-09-252-991A-24900	Sequence 24900, A
34	49	59.0	257	4	US-09-252-991A-31868	Sequence 31868, A
35	49	59.0	326	4	US-09-252-991A-18844	Sequence 18844, A
36	49	59.0	439	4	US-09-252-991A-31919	Sequence 31919, A
37	49	59.0	506	4	US-09-672-785-8	Sequence 8, Appl
38	48	57.8	93	4	US-09-252-991A-29133	Sequence 29133, A
39	48	57.8	172	4	US-09-252-991A-26133	Sequence 26133, A
40	48	57.8	249	4	US-09-252-991A-21189	Sequence 21188, A
41	48	57.8	262	4	US-09-902-540-12987	Sequence 12987, A
42	48	57.8	280	4	US-09-252-991A-17338	Sequence 17338, A
43	48	57.8	311	4	US-09-252-991A-22406	Sequence 22406, A
44	48	57.8	366	6	5470718-4	Patent No. 5470718
45	48	57.8	366	6	5470718-4	Patent No. 5470718

ALIGNMENTS

RESULT 1
US-09-024-975-4
; Sequence 4, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/802,306
; APPLICATION NUMBER:
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-024-975-4

Query Match 100.0%; Score 83; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPLPRRP 14
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Db      1 RRRPRPPYLP RRP 14

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-930-777A-4

Query Match      100.0%; Score 83; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPRPPYLP RRP 14
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Db      1 RRRPRPPYLP RRP 14

RESULT 4
US-08-419-066-2
; Sequence 2, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-930-777A-7

Query Match      100.0%; Score 83; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPRPPYLP RRP 14
        |||||
Db      1 RRRPRPPYLP RRP 14

RESULT 3
US-08-930-777A-4
; Sequence 4, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-2

Query Match          100.0%; Score 83; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14
DB 1 RRRPRPPYLP RPRP 14

RESULT 5
US-09-024-975-2
; Sequence 2, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN W.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-024-975-2

Query Match          100.0%; Score 83; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14
DB 1 RRRPRPPYLP RPRP 14

RESULT 6
US-08-930-777A-2
; Sequence 2, Application US/08930777A

; Patent No. 6713605
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-930-777A-2

Query Match          100.0%; Score 83; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14
DB 1 RRRPRPPYLP RPRP 14

RESULT 7
US-09-739-535-1
; Sequence 1, Application US/09739535
; Patent No. 6794490
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/739,535
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-739-535-1

Query Match          100.0%; Score 83; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RRRPPPYLPRRP 14
DB 1 RRRPPPYLPRRP 14

RESULT 8
US-08-162-052-1
; Sequence 1, Application US/08162052
; Patent No. 5489575
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong-Youn
; APPLICANT: BOMAN, Hans G.
; APPLICANT: MUTT, Viktor
; APPLICANT: JORNVAL, Hans
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,052
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: SE 9101838-2
; FILING DATE: 14-JUN-1991
; APPLICATION DATA:
; APPLICATION NUMBER: WO 92-22578
; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 003300-299
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-162-052-1

Query Match 100.0%; Score 83; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRRP 14
DB 1 RRRPPPYLPRRP 14

RESULT 9
US-08-310-722-1
; Sequence 1, Application US/08310722
; Patent No. 5654273
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,722
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: CMCC379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Boman, Hans G.
; AUTHORS: Mutt, Viktor
; AUTHORS: Jornvall, Hans
; TITLE: No 5654273el Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39

US-08-310-722-1

Query Match 100.0%; Score 83; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRRP 14
DB 1 RRRPPPYLPRRP 14

RESULT 10
US-08-419-066-1
; Sequence 1, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-419-066-1

* Query Match 100.0%; Score 83; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPPYLP RPRP 14
Db 1 RRRPPPPYLP RPRP 14

RESULT 11
US-08-728-333-1
; Sequence 1, Application US/08728333
; Patent No. 5863897
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,333
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,722
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MC00379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Boman, Hans G.
; AUTHORS: Mutt, Viktor
; AUTHORS: Jornvall, Hans
; TITLE: No. 5863897el Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
; US-08-728-333-1

Query Match 100.0%; Score 83; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPPYLP RPRP 14
Db 1 RRRPPPPYLP RPRP 14

RESULT 12
US-09-024-975-1
; Sequence 1, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-024-975-1

Query Match 100.0%; Score 83; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPPYLP RPRP 14
Db 1 RRRPPPPYLP RPRP 14

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; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-930-777A-3

Query Match

Best Local Similarity 81.9%; Score 68; DB 4; Length 23;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PRPPYLPRRP 14

Db 1 PRPPYLPRRP 11

Search completed: October 26, 2005, 05:22:00

Job time : 15.3818 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 05:05:05 ; Search time 51.6727 Seconds
(without alignments)
113.119 Million cell updates/sec

Title: US-10-014-147-7

Perfect score: 83

Sequence: 1 RRRPPVLPYPRP 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	14	14	US-10-014-147-7
2	83	100.0	14	15	US-10-014-147-7
3	83	100.0	15	15	US-10-391-155-3
4	83	100.0	19	14	US-10-014-147-4
5	83	100.0	19	15	US-10-014-147-4
6	83	100.0	26	14	US-10-014-147-2
7	83	100.0	26	15	US-10-014-147-2
8	83	100.0	38	9	US-09-738-742-1
9	83	100.0	38	9	US-09-739-535-1
10	83	100.0	39	14	US-10-014-147-1
11	83	100.0	39	15	US-10-391-155-1

12	83	100.0	39	15	US-10-391-155-2
13	83	100.0	39	15	US-10-391-155-6
14	83	100.0	39	15	US-10-651-147-1
15	83	100.0	42	15	US-10-344-709C-18
16	83	100.0	42	17	US-10-916-185-14
17	83	100.0	42	18	US-10-931-286A-44
18	83	100.0	42	20	US-11-004-379-20
19	68	81.9	23	14	US-10-014-147-3
20	68	81.9	23	15	US-10-651-147-3
21	66	79.5	59	9	US-09-030-619-163
22	66	79.5	59	9	US-09-912-609-51
23	66	79.5	59	15	US-10-277-232-163
24	66	79.5	59	15	US-10-277-233-163
25	66	79.5	59	17	US-10-838-289-683
26	66	79.5	60	16	US-10-344-709C-17
27	64	77.1	11	15	US-10-391-155-4
28	64	77.1	11	18	US-10-502-639-1
29	63.5	76.5	234	16	US-10-425-115-344157
30	59	71.1	11	17	US-10-475-403-5
31	58	69.9	109	16	US-10-767-701-54214
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33	56	67.5	179	16	US-10-425-115-230007
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36	56	67.5	692	11	US-09-758-759-79
37	55	66.3	45	9	US-09-864-761-49065
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44	54	65.1	163	16	US-10-437-963-114067
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ALIGNMENTS

RESULT 1

US-10-014-147-7
; Sequence 7, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A

TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-014-147-7

Query Match 100.0%; Score 83; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRRP 14
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Db 1 RRRPPPYLPRRP 14
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RESULT 2

US-10-651-147-7
Sequence 7, Application US/10651147
Publication No. US2004004334A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/651,147
FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-651-147-7

Query Match 100.0%; Score 83; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRRP 14
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Db 1 RRRPPPYLPRRP 14
|||||

RESULT 3

US-10-391-155-3
Sequence 3, Application US/10391155
Publication No. US20040009463A1
GENERAL INFORMATION:
APPLICANT: Simons, Michael
Gao, Youhe
TITLE OF INVENTION: Method for PR-39 peptide mediated
selective inhibition of IKBA degradation
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia
STATE: Massachusetts
COUNTRY: USA
ZIP: 01930

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: Dell PC
OPERATING SYSTEM: MS XP
SOFTWARE: WordPerfect version 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/391,155
FILING DATE: 18-Mar-2003
CLASSIFICATION: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: B1S-044/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-391-155-3

Query Match 100.0%; Score 83; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRRP 14
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Db 1 RRRPPPYLPRRP 14
|||||

RESULT 4

US-10-014-147-4
Sequence 4, Application US/10014147
Publication No. US20030125249A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-014-147-4
Query Match 100.0%; Score 83; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPRPPYLP RRP 14
DB 1 RRRPRPPYLP RRP 14
RESULT 5
US-10-651-147-4
Sequence 4, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/651,147
FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-651-147-4
Query Match 100.0%; Score 83; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPRPPYLP RRP 14
DB 1 RRRPRPPYLP RRP 14
RESULT 6
US-10-014-147-2
Sequence 2, Application US/10014147
Publication No. US20030125249A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-014-147-2
Query Match 100.0%; Score 83; DB 14; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPRPPYLP RRP 14
DB 1 RRRPRPPYLP RRP 14

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RESULT 7
US-10-651-147-2
; Sequence 2, Application US/10651147
; Publication No. US20040043934A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/651,147
; FILING DATE: 28-Aug-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-651-147-2
Query Match 100.0%; Score 83; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPRPPYLP RPRP 14
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Db 1 RRRPRPPYLP RPRP 14
| | | | | | | | | |
RESULT 8
US-09-738-742-1
; Sequence 1, Application US/09738742
; Publication No. US20020025924A1
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/738,742
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-738-742-1
Query Match 100.0%; Score 83; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPRPPYLP RPRP 14
| | | | | | | | | |
Db 1 RRRPRPPYLP RPRP 14
| | | | | | | | | |
RESULT 9
US-09-739-535-1
; Sequence 1, Application US/09739535
; Publication No. US20020058785A1
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/739,535
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-739-535-1
Query Match 100.0%; Score 83; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPRPPYLP RPRP 14
| | | | | | | | | |
Db 1 RRRPRPPYLP RPRP 14
| | | | | | | | | |
RESULT 10
US-10-014-147-1
; Sequence 1, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
```

REFERENCE/DOCKET NUMBER: 23625-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (816) 474-9050

TELEFAX: (816) 474-9057

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-014-147-1

Query Match 100.0%; Score 83; DB 14; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.0084;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RRP 14

|||||

Db 1 RRRPRPPYLP RRP 14

RESULT 11

US-10-391-155-1

Sequence 1, Application US/10391155

Publication No. US20040009463A1

GENERAL INFORMATION:

APPLICANT: Simons, Michael

Gao, Youhe

TITLE OF INVENTION: Method for PR-39 peptide mediated

selective inhibition of IKBA degradation

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: David Prashker, Esq.

STREET: P.O. Box 5387

CITY: Magnolia

STATE: Massachusetts

COUNTRY: USA

ZIP: 01930

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage

COMPUTER: Dell PC

OPERATING SYSTEM: MS XP

SOFTWARE: WordPerfect version 10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/391.155

FILING DATE: 18-Mar-2003

CLASSIFICATION: Unknown

ATTORNEY/AGENT INFORMATION:

NAME: David Prashker, Esq.

REGISTRATION NUMBER: 29,693

REFERENCE/DOCKET NUMBER: BIS-044/D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (978) 525-3794

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-391-155-1

Query Match 100.0%; Score 83; DB 15; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.0084;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RRP 14

|||||

Db 1 RRRPRPPYLP RRP 14

RESULT 12

US-10-391-155-2

Sequence 2, Application US/10391155

Publication No. US20040009463A1

GENERAL INFORMATION:

APPLICANT: Simons, Michael

Gao, Youhe

TITLE OF INVENTION: Method for PR-39 peptide mediated

selective inhibition of IKBA degradation

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: David Prashker, Esq.

STREET: P.O. Box 5387

CITY: Magnolia

STATE: Massachusetts

COUNTRY: USA

ZIP: 01930

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage

COMPUTER: Dell PC

OPERATING SYSTEM: MS XP

SOFTWARE: WordPerfect version 10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/391.155

FILING DATE: 18-Mar-2003

CLASSIFICATION: Unknown

ATTORNEY/AGENT INFORMATION:

NAME: David Prashker, Esq.

REGISTRATION NUMBER: 29,693

REFERENCE/DOCKET NUMBER: BIS-044/D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (978) 525-3794

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-391-155-2

Query Match 100.0%; Score 83; DB 15; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.0084;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RRP 14

|||||

Db 1 RRRPRPPYLP RRP 14

RESULT 13

US-10-391-155-6

Sequence 6, Application US/10391155

Publication No. US20040009463A1

GENERAL INFORMATION:

APPLICANT: Simons, Michael

Gao, Youhe

TITLE OF INVENTION: Method for PR-39 peptide mediated

selective inhibition of IKBA degradation

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: David Prashker, Esq.

STREET: P.O. Box 5387

CITY: Magnolia

STATE: Massachusetts

COUNTRY: USA

ZIP: 01930

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage

COMPUTER: Dell PC

OPERATING SYSTEM: MS XP

SOFTWARE: WordPerfect version 10

Search completed: October 26, 2005, 05:29:00
Job time : 53.6727 secs